

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 44.6154 Seconds  
(without alignments)  
64.324 Million cell updates/sec

Title: US-09-574-735C-34

Perfect score: 38

Sequence: 1 FXXKYNFD 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	36	94.7	8	5	ABG65707	Plant	ICK
2	36	94.7	8	5	ABG65702	Plant	ICK
3	36	94.7	8	5	ABG65706	Plant	ICK
4	36	94.7	37	3	AP01950	Rice	Cycl
5	36	94.7	37	3	AP01950	Rice	Cycl
6	36	94.7	42	6	ABE98860	Maize	CKI
7	36	94.7	46	6	ABE98862	Maize	CKI
8	36	94.7	53	3	AB26245	Corn	Cycl
9	36	94.7	53	3	AP01940	Corn	Cycl
10	36	94.7	116	5	ABG65674	Corn	ICK
11	36	94.7	125	5	AB26250	Corn	Cycl
12	36	94.7	126	3	AB26249	Corn	Cycl
13	36	94.7	226	5	ABG65692	Rice	Osic
14	36	94.7	256	6	ABE98757	Maize	CKI
15	36	94.7	262	5	ABG65670	Osic	2 p
16	35	92.1	8	5	ABG65701	Plant	ICK
17	35	92.1	196	3	AY44340	Chenopodi	
18	35	92.1	196	3	AY44340	Chenopodi	
19	35	92.1	196	5	AAE25108	Chenopodi	
20	35	92.1	440	5	ABG69080	Botulinum	
21	35	92.1	441	5	ABG69070	Botulinum	
22	35	92.1	824	5	ABG69081	Botulinum	
23	35	92.1	825	8	ADN11038	Clostridi	
24	35	92.1	1664	5	ABr53595	Protein s	
25	35	92.1	1664	7	ADK64734	Disease t	

ALIGNMENTS

RESULT 1

ABG65707

ID ABG65707 standard; peptide; 8 AA.

XX

AC ABG65707;

XX

DT 27-AUG-2002 (first entry)

XX

DE Plant ICK protein conserved motif 1 #15.

XX

KW Plant; inhibitor of cyclin dependent kinase; ICK.

XX

OS Zea mays.

XX

PN WO200228893-A2.

XX

PD 11-APR-2002.

XX

PF 29-JUN-2001; 2001WO-IB001492.

XX

PR 14-JUL-2000; 2000US-0218471P.

XX

PR 13-OCT-2000; 2000US-0241219P.

XX

XX (CROP-) CROPDESIGN NV.

PA

XX Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;

XX

PI Hatzfeld Y;

XX

XX WPI; 2002-471311/50.

DR

XX

XX

PT

PT

PT

PT

XX

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

XX

```

SQ      Sequence 8 AA;
Query Match          94.7%; Score 36; DB 5; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FXXKYNFD 8
DB      1 FASKYNFD 8

RESULT 2
ABG65702
ID      ABG65702 standard; peptide; 8 AA.
XX
AC      ABG65702;
XX
DT      27-AUG-2002 (first entry)
XX
DE      Plant ICK protein conserved motif 1 #10.
XX
KW      Plant; inhibitor of cyclin dependent kinase; ICK.
XX
OS      Oryza sativa.
XX
PN      WO200228893-A2.
XX
PD      11-APR-2002.
XX
PF      29-JUN-2001; 2001WO-IB001492.
XX
PR      14-JUL-2000; 2000US-0218471P.
XX
PR      13-OCT-2000; 2000US-0241219P.
XX
PA      (CROP-) CROPDESIGN NV.
XX
PI      Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
PI      Hatzfeld Y;
XX
XX      WPI; 2002-471311/50.
XX
PT      Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
PT      to screen substrates, drugs or compounds which modulate ICK activity and
PT      treat disorders characterized by an insufficient or excessive production
PT      of ICK inhibitors.
XX
PS      Disclosure; Page 14; 141pp; English.
XX
CC      This invention relates to the DNA and protein sequences of novel isolated
CC      ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
CC      the invention may be used for treating disorders characterised by
CC      insufficient or excessive production of an ICK inhibitor. The protein of
CC      the invention may also be used to screen for naturally-occurring ICK
CC      substrates, drugs or compounds which modulate ICK activity, as well as to
CC      treat disorders characterised by insufficient or excessive production of
CC      ICK protein, forms which have decreased or aberrant activity compared to
CC      ICK wild type protein. The present sequence represents an inhibitor of
CC      cyclin dependent kinase (ICK) protein of the invention
XX
SQ      Sequence 8 AA;
Query Match          94.7%; Score 36; DB 5; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FXXKYNFD 8
DB      1 FASKYNFD 8

RESULT 3
ABG65706
ID      ABG65706 standard; peptide; 8 AA.
XX
AC      ABG65706;
XX
DT      01-NOV-2001 (first entry)
XX
DE      Rice Cyclin dependent kinase inhibitor (CDKI) clone rds2c.pk0088.c24.
XX
KW      Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; rice;
KW      plant growth inhibitor.
XX
OS      Oryza sativa.
XX
XX      Key
XX      Misc-difference 33
XX      Location/Qualifiers
XX      FT

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FT XX /note= "Encoded by GTCA"
PN XX
XX WO200060087-A2.
XX 12-OCT-2000.
XX PD
XX PF
XX WO200060087-A2.
XX 06-APR-2000; 2000WO-US009106.
XX PR
XX 07-APR-1999; 99US-0128192P.
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PI Klein TM, Weng Z, Cahoon RE;
XX WPI; 2000-679375/66.
XX N-PSDB; AAN02400.
XX Cyclin dependent kinase inhibitor sequences, useful for identifying
XX herbicides and plant growth inhibitors.
XX Claim 10; Fig 1; 58pp; English.
XX The invention describes a novel isolated polynucleotide comprising a
XX nucleotide sequence encoding one of 17 specific cyclin dependent kinase
XX inhibitor (CDKI) polypeptides, cell cycle regulators involved in control
XX of cell division, growth and death. The nucleotide sequences can be used
XX in a vector to transform a host cell to produce the CDKI polypeptide.
XX They can also be used in methods for selecting and obtaining a nucleic
XX acid sequence that encodes CDKI or affects the level of CDKI expression.
XX The encoded protein can be used in a method for evaluating a compound for
XX its ability to inhibit the activity of a CDKI. The inhibitors can be used
XX as herbicides. They can also be used to inhibit plant growth. The
XX polynucleotide sequences can be used in gene mapping and as genetic
XX markers. The sequence is the rice CDKI clone rds2c.pk008.024 as described
XX in the method of the invention
XX SQ Sequence 37 AA;
XX Query Match 94.7%; Score 36; DB 3; Length 37;
XX Best Local Similarity 75.0%; Pred. No. 2.1;
XX Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 FXXXYNFD 8
XX | | | | |
XX 8 FAAKYNFD 15
XX Db
XX
XX RESULT 6
XX ABB98860
XX ID ABB98860 standard; protein; 42 AA.
XX AC ABB98860;
XX DT 21-FEB-2003 (first entry)
XX DE Maize CKI_B C-terminal protein fragment.
XX KW Maize; cyclin-dependent kinase inhibitor; CKI; plant; corn; crop yield;
XX root size; plant growth; tassel size; ear size; male sterility;
XX endoreduplication.
XX OS Zea mays.
XX PN WO200281623-A2.
XX PD 17-OCT-2002.
XX PF 06-NOV-2001; 2001WO-US044038.
XX PR 07-NOV-2000; 2000US-0246349P.
XX PA (PION-) PIONEER HI-BRED INT INC.
XX ARIZ-) ARIZONA BOARD OF REGENTS.
XX PI Gordon-Kamm WJ, Lowe KS, Larkins BA, Dilkes BR, Sun Y;
XX WPI; 2003-058511/05.
XX Novel cyclin-dependent kinase polynucleotides and their encoded proteins,
XX involved in cell cycle regulation, and useful for altering cell cycle
XX protein content, cell cycle progression, cell number and composition of
XX plants.
XX Example 11; Page 46; 69pp; English.
XX The present invention relates to maize cyclin-dependent kinase inhibitor

```

CC (CKI), CKI\_B, CKI\_C and CKI\_D. The coding sequences (I) for these  
 CC proteins are useful for modulating the activity of CDK in a plant such as  
 CC a corn, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton,  
 CC rice, barley, oil-seed Brassica and millet. Modulating the activity of  
 CC CDK, preferably modulating downward is useful for providing differential  
 CC growth in a plant, especially a positive growth advantage and modulating  
 CC CDK activity upward is useful for increasing crop yield, root size, plant  
 CC growth, tassel size and/or ear size. Modulating CDK activity is also  
 CC useful for conferring male sterility and for improving transformation  
 CC frequencies by increasing the number of cells in cell division. CDK  
 CC activity can also be modulated for modulating endoreduplication in the  
 CC endosperm of corn, sorghum, wheat, rice, barley, and millet, where the  
 CC promoter used is an endosperm-preferred promoter. The cell numbers are  
 CC modulated in one or more tissues of a plant, comprising root, seed,  
 CC tassel, ear, silk, stalk, embryo, flower, grain, germ, head, leaves,  
 CC stem, seed, trunk, meristem or fruit. The cells are nucleus, endosperm,  
 CC pericarp, meristematic or leaf cells. (I) is also useful for identifying  
 CC maize CKI interacting proteins, by adding the nucleic acid sequence to  
 CC a second nucleic acid sequence encoding a DNA-binding domain. The present  
 CC sequence is a C-terminal protein fragment of CKI\_B. This sequence  
 CC contains a CDK binding region and/or cyclin binding domains  
 CC  
 XX  
 SQ Sequence 42 AA;

Query Match 94.7%; Score 36; DB 6; Length 42;  
 Best Local Similarity 75.0%; Pred. No. 2.4;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 FXXKYNFD 8  
 DB 14 FASKYNFD 21

RESULT 7  
 ABB98862  
 ID ABB98862 standard; protein; 46 AA.  
 XX  
 AC ABB98862;  
 XX  
 DT 21-FEB-2003 (first entry)  
 XX  
 DE Maize CKI\_D C-terminal protein fragment.  
 XX  
 KW Maize; cyclin-dependent kinase inhibitor; CKI; plant; corn; crop yield;  
 KW root size; plant growth; tassel size; ear size; male sterility;  
 KW endoreduplication.  
 XX  
 OS Zea mays.  
 XX  
 PN WO200281623-A2.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 06-NOV-2001; 2001WO-US044038.  
 XX  
 PR 07-NOV-2000; 2000US-0246349P.  
 XX  
 PA (PION-) PIONEER HI-BRED INT INC.  
 PA (ARIZ-) ARIZONA BOARD OF REGENTS.  
 XX  
 PI Gordon-Kamm WJ, Lowe KS, Larkins BA, Dilkes BR, Sun Y;  
 XX WPI; 2003-058511/05.  
 XX  
 PT Novel cyclin-dependent kinase polynucleotides and their encoded proteins,  
 PT involved in cell cycle regulation, and useful for altering cell cycle  
 PT protein content, cell cycle progression, cell number and composition of  
 PT plants.  
 XX  
 PS Example 11; Page 46; 69pp; English.  
 XX  
 PS The present invention relates to maize cyclin-dependent kinase inhibitor  
 CC (CKI), CKI\_B, CKI\_C and CKI\_D. The coding sequences (I) for these

CC proteins are useful for modulating the activity of CDK in a plant such as  
 CC a corn, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton,  
 CC rice, barley, oil-seed Brassica and millet. Modulating the activity of  
 CC CDK, preferably modulating downward is useful for providing differential  
 CC growth in a plant, especially a positive growth advantage and modulating  
 CC CDK activity upward is useful for increasing crop yield, root size, plant  
 CC growth, tassel size and/or ear size. Modulating CDK activity is also  
 CC useful for conferring male sterility and for improving transformation  
 CC frequencies by increasing the number of cells in cell division. CDK  
 CC activity can also be modulated for modulating endoreduplication in the  
 CC endosperm of corn, sorghum, wheat, rice, barley, and millet, where the  
 CC promoter used is an endosperm-preferred promoter. The cell numbers are  
 CC modulated in one or more tissues of a plant, comprising root, seed,  
 CC tassel, ear, silk, stalk, embryo, flower, grain, germ, head, leaves,  
 CC stem, seed, trunk, meristem or fruit. The cells are nucleus, endosperm,  
 CC pericarp, meristematic or leaf cells. (I) is also useful for identifying  
 CC maize CKI interacting proteins, by adding the nucleic acid sequence to  
 CC a second nucleic acid sequence encoding a DNA-binding domain. The present  
 CC sequence is a C-terminal protein fragment of CKI\_D. This sequence  
 CC contains a CDK binding region and/or cyclin binding domains  
 CC  
 XX  
 SQ Sequence 46 AA;

Query Match 94.7%; Score 36; DB 6; Length 46;  
 Best Local Similarity 75.0%; Pred. No. 2.6;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 FXXKYNFD 8  
 DB 19 FASKYNFD 26

RESULT 8  
 AAB26245  
 ID AAB26245 standard; protein; 53 AA.  
 XX  
 AC AAB26245;  
 XX  
 DT 17-JAN-2001 (first entry)  
 XX  
 DE Corn cyclin-dependent kinase inhibitor #1.  
 XX  
 KW Corn; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division;  
 KW cell growth; herbicide.  
 XX  
 OS Zea mays.  
 XX  
 PN WO200060087-A2.  
 XX  
 PD 12-OCT-2000.  
 XX  
 PF 06-APR-2000; 2000WO-US009106.  
 XX  
 PR 07-APR-1999; 99US-0128192P.  
 XX  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Klein TM, Weng Z, Cahoon RE;  
 XX WPI; 2000-679375/66.  
 DR N-PSDB; AAA95276.  
 XX  
 PT Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.  
 PS Claim 10; Page 40; 58pp; English.  
 XX  
 CC The present sequence is the corn cyclin-dependent kinase inhibitor  
 CC (CDKI), its coding sequence was isolated by searching a corn silk cDNA  
 CC library for sequences similar to those encoding the CDKI from *Chenopodium*  
 CC rubrum, *Caenorhabditis elegans* and *Arabidopsis thaliana*. CDKI is involved  
 CC in the cell cycle, and may promote or inhibit cell division and growth.  
 CC The protein and its coding sequence are useful in the production of



CC transgenic plants which produce increased or decreased amounts of the  
 CC CDKI protein, in the identification of herbicides, in genetic and  
 CC physical mapping and in the isolation of the CDKI gene in other organisms  
 XX  
 SQ Sequence 53 AA;

Query Match 94.7%; Score 36; DB 3; Length 53;  
 Best Local Similarity 75.0%; Pred. No. 3;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 FXXKYNFD 8  
 | | | | |  
 Db 30 FASKYNFD 37

RESULT 9  
 AAP01940  
 ID AAP01940 standard; protein; 53 AA.  
 AC AAP01940;  
 XX  
 XX 01-NOV-2001 (first entry)  
 DT  
 DE Corn Cyclin dependent kinase inhibitor (CDKI) clone csln.pk0050.e6.  
 XX  
 XX Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; corn;  
 KW plant growth inhibitor.  
 XX  
 XX Zea mays.  
 OS  
 XX WO2000060087-A2.  
 PN  
 XX 12-OCT-2000.  
 PD  
 XX 06-APR-2000; 2000WO-US009106.  
 PF  
 XX 07-APR-1999; 99US-0128192P.  
 PR  
 XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PA  
 XX Klein TM, Wang Z, Cahoon RE;  
 PI  
 XX WPI; 2000-679375/66.  
 DR  
 XX N-PSDB; AAN02390.  
 DR  
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.  
 XX  
 PS Claim 10; Page 40; 58pp; English.

The invention describes a novel isolated polynucleotide comprising a  
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase  
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control  
 CC of cell division, growth and death. The nucleotide sequences can be used  
 CC in a vector to transform a host cell to produce the CDKI polypeptide.  
 CC They can also be used in methods for selecting and obtaining a nucleic  
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.  
 CC The encoded protein can be used in a method for evaluating a compound for  
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used  
 CC as herbicides. They can also be used to inhibit plant growth. The  
 CC polynucleotide sequences can be used in gene mapping and as genetic  
 CC markers. The sequence is the corn CDKI clone csln.pk0050.e6 as described  
 CC in the method of the invention

SQ Sequence 53 AA;  
 Query Match 94.7%; Score 36; DB 3; Length 53;  
 Best Local Similarity 75.0%; Pred. No. 3;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 FXXKYNFD 8  
 | | | | |  
 Db 30 FASKYNFD 37

RESULT 10  
 ABG65674  
 ID ABG65674 standard; protein; 116 AA.  
 XX

AC ABG65674;  
 XX  
 XX 07-AUG-2003 (revised)  
 DT 27-AUG-2002 (first entry)  
 XX  
 XX Corn ICK 1 protein.  
 DE  
 XX Plant; inhibitor of cyclin dependent kinase; ICK.  
 KW  
 XX Zea mays.  
 OS

XX WO200228893-A2.  
 PN  
 XX 11-APR-2002.  
 PD  
 XX 29-JUN-2001; 2001WO-IB001492.  
 PF  
 XX 14-JUL-2000; 2000US-0218471P.  
 PR  
 XX 13-OCT-2000; 2000US-0241219P.  
 PR  
 XX (CROP-) CROPDESIGN NV.  
 PA

XX Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;  
 PI Hatzfeld Y;  
 PI  
 XX WPI; 2002-471311/50.  
 DR  
 XX N-PSDB; ABK93954.  
 DR

XX Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used  
 PT to screen substrates, drugs or compounds which modulate ICK activity and  
 PT treat disorders characterized by an insufficient or excessive production  
 PT of ICK inhibitors.  
 XX

PS Claim 48; Fig 4; 141pp; English.

XX This invention relates to the DNA and protein sequences of novel isolated  
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of  
 CC the invention may be used for treating disorders characterised by  
 CC insufficient or excessive production of an ICK inhibitor. The protein of  
 CC the invention may also be used to screen for naturally-occurring ICK  
 CC substrates, drugs or compounds which modulate ICK activity, as well as to  
 CC treat disorders characterised by insufficient or excessive production of  
 CC ICK protein, forms which have decreased or aberrant activity compared to  
 CC ICK wild type protein. The present sequence represents an inhibitor of  
 CC cyclin dependent kinase (ICK) protein of the invention. (Updated on 07-  
 CC AUG-2003 to correct OS field.)

XX Sequence 116 AA;

Query Match 94.7%; Score 36; DB 5; Length 116;  
 Best Local Similarity 75.0%; Pred. No. 7;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
 | | | | |  
 Db 89 FASKYNFD 96

RESULT 11  
 AAB26250  
 ID AAB26250 standard; protein; 125 AA.  
 XX

XX AAB26250;  
 XX

XX 17-JAN-2001 (first entry)  
 DT  
 XX Corn cyclin-dependent kinase inhibitor #3.  
 DE

XX Corn; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division;  
 KW cell growth; herbicide.  
 XX  
 OS Zea mays.  
 XX WO2000060087-A2.  
 XX  
 XX 12-OCT-2000.  
 XX  
 XX 06-APR-2000; 2000WO-US009106.  
 XX  
 XX 07-APR-1999; 99US-0128192P.  
 XX  
 XX (DUPO) DU PONT DE NEMOURS & CO E I.  
 XX  
 XX Klein TM, Weng Z, Cahoon RE;  
 PI WPI; 2000-679375/66.  
 XX N-PSDB; AAA95281.  
 XX  
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.  
 XX  
 XX Claim 10; Fig 1; 58pp; English.  
 XX  
 XX The present sequence is the corn cyclin-dependent kinase inhibitor  
 CC (CDKI). Its coding sequence was isolated by searching a contig comprising  
 CC cDNA from corn roots and ear leaf sheath for sequences similar to those  
 CC encoding the CDKI from *Chenopodium rubrum*, *Caenorhabditis elegans* and  
 CC *Arabidopsis thaliana*. CDKI is involved in the cell cycle, and may promote  
 CC or inhibit cell division and growth. The protein and its coding sequence  
 CC are useful in the production of transgenic plants which produce increased  
 CC or decreased amounts of the CDKI protein, in the identification of  
 CC herbicides, in genetic and physical mapping and in the isolation of the  
 CC CDKI gene in other organisms  
 XX  
 XX Sequence 125 AA;  
 Query Match 94.7%; Score 36; DB 3; Length 125;  
 Best Local Similarity 75.0%; Pred. No. 7.6;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 FXXKYNFED 8  
 DB 97 FASKYNFD 104  
 RESULT 12  
 ID AAB26249 standard; protein; 126 AA.  
 XX  
 XX AAB26249;  
 AC  
 XX 17-JAN-2001 (first entry)  
 DT  
 XX Corn cyclin-dependent kinase inhibitor #2.  
 DE  
 XX Corn; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division;  
 KW cell growth; herbicide.  
 XX  
 XX Zea mays.  
 XX WO2000060087-A2.  
 XX  
 XX 12-OCT-2000.  
 XX  
 XX 06-APR-2000; 2000WO-US009106.  
 XX  
 XX 07-APR-1999; 99US-0128192P.  
 XX  
 XX (DUPO) DU PONT DE NEMOURS & CO E I.

PI Klein TM, Weng Z, Cahoon RE;  
 XX WPI; 2000-679375/66.  
 DR N-PSDB; AAA95280.  
 XX  
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.  
 XX  
 XX Claim 10; Fig 1; 58pp; English.  
 XX  
 XX The present sequence is the corn cyclin-dependent kinase inhibitor  
 CC (CDKI). Its coding sequence was isolated by searching a corn silk cDNA  
 CC library for sequences similar to those encoding the CDKI from *Chenopodium*  
 CC *rubrum*, *Caenorhabditis elegans* and *Arabidopsis thaliana*. CDKI is involved  
 CC in the cell cycle, and may promote or inhibit cell division and growth.  
 CC The protein and its coding sequence are useful in the production of  
 CC transgenic plants which produce increased or decreased amounts of the  
 CC CDKI protein, in the identification of herbicides, in genetic and  
 CC physical mapping and in the isolation of the CDKI gene in other organisms  
 XX  
 XX Sequence 126 AA;  
 Query Match 94.7%; Score 36; DB 3; Length 126;  
 Best Local Similarity 75.0%; Pred. No. 7.7;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 FXXKYNFED 8  
 DB 99 FASKYNFD 106  
 RESULT 13  
 ID AAG65692 standard; protein; 226 AA.  
 XX  
 XX AAG65692;  
 AC  
 XX 27-AUG-2002 (first entry)  
 DT  
 XX Rice OsICK5 protein.  
 DE  
 XX Plant; inhibitor of cyclin dependent kinase; ICK.  
 KW  
 XX  
 XX Oryza sativa.  
 OS  
 XX WO200228893-A2.  
 PN  
 XX 11-APR-2002.  
 PD  
 XX 29-JUN-2001; 2001WO-IB001492.  
 PF  
 XX 14-JUL-2000; 2000US-0218471P.  
 PR  
 XX 13-OCT-2000; 2000US-0241219P.  
 PR  
 XX (CROP-) CROPDESIGN NV.  
 PA  
 XX Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;  
 PI Hatzfeld Y;  
 XX  
 XX WPI; 2002-471311/50.  
 DR N-PSDB; ABK93981.  
 DR  
 XX Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used  
 PT to screen substrates, drugs or compounds which modulate ICK activity and  
 PT treat disorders characterized by an insufficient or excessive production  
 PT of ICK inhibitors.  
 XX  
 XX Claim 48; Page 139-140; 141pp; English.  
 PS  
 XX This invention relates to the DNA and protein sequences of novel isolated  
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of  
 CC the invention may be used for treating disorders characterised by  
 CC insufficient or excessive production of an ICK inhibitor. The protein of

CC the invention may also be used to screen for naturally-occurring ICK  
 CC substrates, drugs or compounds which modulate ICK activity, as well as to  
 CC treat disorders characterised by insufficient or excessive production of  
 CC ICK protein, forms which have decreased or aberrant activity compared to  
 CC ICK wild type protein. The present sequence represents an inhibitor of  
 CC cyclin dependent kinase (ICK) protein of the invention  
 CC  
 XX Sequence 226 AA;

Query Match 94.7%; Score 36; DB 5; Length 226;  
 Best Local Similarity 75.0%; Pred. No. 14;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXKYNFD 8  
 | | | | |  
 Db 196 FAKYNFD 203

## RESULT 14

ABB98757  
 ID ABB98757 standard; protein; 256 AA.

XX AC ABB98757;

XX DT 21-FEB-2003 (first entry)

XX DE Maize CKI\_B.

XX KW Maize; cyclin-dependent kinase inhibitor; CKI; CKI\_B; plant; corn;  
 KW crop yield; root size; plant growth; tassel size; ear size;  
 KW male sterility; endoreduplication.

XX OS Zea mays.

XX FH Key Location/Qualifiers  
 FT Domain 1..7  
 FT /note= "Conserved domain"

XX FN WO200281623-A2.

XX PD 17-OCT-2002.

XX XX 06-NOV-2001; 2001WO-US044038.

XX PR 07-NOV-2000; 2000US-0245349P.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX FA (ARIZ-) ARIZONA BOARD OF REGENTS.

XX FI Gordon-Kamm WJ, Lowe KS, Larkins BA, Dilkes BR, Sun Y;

XX DR WPI; 2003-050511/05.

XX DR N-PSDB; ABV74603.

XX PT Novel cyclin-dependent kinase polynucleotides and their encoded proteins,  
 PT involved in cell cycle regulation, and useful for altering cell cycle  
 PT protein content, cell cycle progression, cell number and composition of  
 PT plants.

XX PS Claim 12; Page 65-66; 69pp; English.

XX CC The present sequence is maize cyclin-dependent kinase inhibitor (CKI),  
 CC CKI\_B. The coding sequence for this protein (I) is useful for modulating  
 CC the activity of cyclin-dependent kinase (CDK) in a plant such as a corn,  
 CC soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice,  
 CC barley, oil-seed Brassica and millet. Modulating the activity of CDK,  
 CC preferably modulating downward is useful for providing differential  
 CC growth in a plant, especially a positive growth advantage and modulating  
 CC CDK activity upward is useful for increasing crop yield, root size, plant  
 CC growth, tassel size and/or ear size. Modulating CDK activity is also  
 CC useful for conferring male sterility and for improving transformation  
 CC frequencies by increasing the number of cells in cell division. CDK  
 CC activity can also be modulated for modulating endoreduplication in the

CC endosperm of corn, sorghum, wheat, rice, barley, and millet, where the  
 CC promoter used is an endosperm-preferred promoter. The cell numbers are  
 CC modulated in one or more tissues of a plant, comprising root, seed,  
 CC tassel, ear, silk, stalk, embryo, flower, grain, germ, head, leaves,  
 CC stem, seed, trunk, meristem or fruit. The cells are nucleus, endosperm,  
 CC pericarp, meristematic or leaf cells. (I) is also useful for identifying  
 CC maize CKI interacting proteins, by adducting the nucleic acid sequence to  
 CC a second nucleic acid sequence encoding a DNA-binding domain  
 CC  
 XX Sequence 256 AA;

Query Match 94.7%; Score 36; DB 6; Length 256;  
 Best Local Similarity 75.0%; Pred. No. 16;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXKYNFD 8  
 | | | | |  
 Db 228 FASKYNFD 235

## RESULT 15

ABG65670

ID ABG65670 standard; protein; 262 AA.

XX AC ABG65670;

XX DT 27-AUG-2002 (first entry)

XX DE OsICK 2 protein.

XX KW Plant; inhibitor of cyclin dependent kinase; ICK.

XX OS Oryza sativa.

XX PN WO200228893-A2.

XX PD 11-APR-2002.

XX PF 29-JUN-2001; 2001WO-IB001492.

XX PR 14-JUL-2000; 2000US-0218471P.

XX PR 13-OCT-2000; 2000US-0241219P.

XX XX (CROP-) CROPDDESIGN NV.

XX PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;

XX PI Hatzfeld Y;

XX DR WPI; 2002-471311/50.

XX DR N-PSDB; ABX93958.

XX PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used  
 PT to screen substrates, drugs or compounds which modulate ICK activity and  
 PT treat disorders characterized by an insufficient or excessive production  
 PT of ICK inhibitors.

XX PS Claim 48; Fig 3; 141pp; English.

XX CC This invention relates to the DNA and protein sequences of novel isolated  
 CC ICK (inhibitors of Cyclin Dependent Kinases) proteins. The sequences of  
 CC the invention may be used for treating disorders characterised by  
 CC insufficient or excessive production of an ICK inhibitor. The protein of  
 CC the invention may also be used to screen for naturally-occurring ICK  
 CC substrates, drugs or compounds which modulate ICK activity, as well as to  
 CC treat disorders characterised by insufficient or excessive production of  
 CC ICK protein, forms which have decreased or aberrant activity compared to  
 CC ICK wild type protein. The present sequence represents an inhibitor of  
 CC cyclin dependent kinase (ICK) protein of the invention  
 CC  
 XX Sequence 262 AA;

Query Match 94.7%; Score 36; DB 5; Length 262;  
 Best Local Similarity 75.0%; Pred. No. 17;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 FXXKYNFD 8  
| | | | |  
Db 233 FAKYNFD 240

Search completed: October 26, 2004, 15:36:51  
Job time : 45.6154 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 13.2308 Seconds  
(without alignments)  
40.099 Million cell updates/sec

Title: US-09-574-735C-34  
Perfect score: 38  
Sequence: 1 FXXKYNFD 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	89.5	222	4	US-09-526-597D-4
2	34	89.5	223	4	US-09-526-597D-6
3	31	81.6	118	4	US-09-248-796A-18335
4	31	81.6	385	4	US-09-248-796A-16581
5	31	81.6	648	4	US-09-538-092-536
6	31	81.6	814	1	US-08-233-788A-42
7	30	78.9	85	4	US-09-270-767-61052
8	30	78.9	147	4	US-09-270-767-32252
9	30	78.9	147	4	US-09-270-767-47469
10	30	78.9	170	4	US-09-270-767-34019
11	30	78.9	170	4	US-09-270-767-49236
12	30	78.9	209	4	US-09-526-597D-2
13	30	78.9	348	4	US-09-328-352-7509
14	30	78.9	363	4	US-09-270-767-45543
15	30	78.9	410	3	US-09-140-466-2
16	30	78.9	682	4	US-09-252-991A-30482
17	30	78.9	1835	3	US-09-404-650-5
18	30	78.9	1835	4	US-09-495-541-2
19	30	78.9	1912	4	US-09-495-714C-2
20	30	78.9	1968	1	US-07-745-206A-7
21	30	78.9	1968	1	US-08-455-543A-45
22	30	78.9	1968	2	US-08-223-305C-45
23	30	78.9	1968	2	US-08-311-363-7
24	30	78.9	1977	4	US-09-495-714C-4
25	30	78.9	1985	4	US-09-495-714C-6
26	30	78.9	2161	1	US-07-745-206A-2
27	30	78.9	2161	1	US-08-455-543A-49

28 30 78.9 2161 1 US-08-455-543A-51 Sequence 51, Appl  
29 30 78.9 2161 2 US-08-223-305C-49 Sequence 49, Appl  
30 30 78.9 2161 2 US-08-223-305C-51 Sequence 51, Appl  
31 30 78.9 2161 2 US-08-311-363-2 Sequence 2, Appl  
32 30 78.9 2175 3 US-09-404-650-2 Sequence 2, Appl  
33 30 78.9 2175 4 US-09-935-541-2 Sequence 2, Appl  
34 30 78.9 2188 3 US-08-404-650-4 Sequence 4, Appl  
35 30 78.9 2188 4 US-09-935-541-4 Sequence 4, Appl  
36 30 78.9 2273 3 US-09-426-998-5 Sequence 5, Appl  
37 30 78.9 2353 3 US-08-984-709A-50 Sequence 50, Appl  
38 30 78.9 2516 3 US-08-374-077C-2 Sequence 2, Appl  
39 30 78.9 2516 3 US-08-895-590-2 Sequence 2, Appl  
40 30 78.9 2516 4 US-09-538-879A-2 Sequence 2, Appl  
41 29 76.3 134 4 US-09-248-796A-22886 Sequence 22886, A  
42 29 76.3 134 4 US-09-164-615-5 Sequence 5, Appl  
43 29 76.3 373 3 US-09-039-198A-14 Sequence 14, Appl  
44 29 76.3 373 3 US-09-039-198A-15 Sequence 15, Appl  
45 29 76.3 373 3 US-08-877-599-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-09-526-597D-4  
; Sequence 4, Application US/09526597D  
; Patent No. 6710227  
; GENERAL INFORMATION:  
; APPLICANT: De Veylder, Lieven  
; APPLICANT: De Almeida, Janice  
; APPLICANT: Landrieu, Isabelle  
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof  
; FILE REFERENCE: 1187-2  
; CURRENT APPLICATION NUMBER: US/09/526,597D  
; CURRENT FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 4  
; LENGTH: 222  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; US-09-526-597D-4

Query Match 89.5%; Score 34; DB 4; Length 222;  
Best Local Similarity 75.0%; Pred. No. 9.2;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXKYNFD 8  
Db 197 FXXKYNFD 204

RESULT 2  
US-09-526-597D-6  
; Sequence 6, Application US/09526597D  
; Patent No. 6710227  
; GENERAL INFORMATION:  
; APPLICANT: De Veylder, Lieven  
; APPLICANT: De Almeida, Janice  
; APPLICANT: Landrieu, Isabelle  
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof  
; FILE REFERENCE: 1187-2  
; CURRENT APPLICATION NUMBER: US/09/526,597D  
; CURRENT FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 6  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; US-09-526-597D-6

Query Match 89.5%; Score 34; DB 4; Length 223;

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Best Local Similarity 75.0%; Pred. No. 9.2;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
Db 198 FMEKYNFD 205

RESULT 3
US-09-248-796A-18335
; Sequence 18335, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18335
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18335

Query Match 81.6%; Score 31; DB 4; Length 118;
Best Local Similarity 62.5%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
Db 34 FLSKFNFD 41

RESULT 4
US-09-248-796A-16581
; Sequence 16581, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16581
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16581

Query Match 81.6%; Score 31; DB 4; Length 385;
Best Local Similarity 62.5%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
Db 106 FNDKYNFD 113

RESULT 5
US-09-538-092-536
; Sequence 536, Application US/09538092
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Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 536
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YLR098C
US-09-538-092-536

Query Match 81.6%; Score 31; DB 4; Length 648;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
Db 620 FALRYNFD 627

RESULT 6
US-08-233-788A-42
; Sequence 42, Application US/08233788A
; Patent No. 5635617
; GENERAL INFORMATION:
; APPLICANT: Doran, James L.
; APPLICANT: Kay, William W.
; APPLICANT: Collinson, Karen S.
; APPLICANT: Clouthier, Sharon C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
; OF SALMONELLA
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,788A
; FILING DATE: 26-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: King, Joshua
; REGISTRATION NUMBER: 35,570
; REFERENCE/DOCKET NUMBER: 920043.403C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 814 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-233-788A-42

Query Match      81.6%; Score 31; DB 1; Length 814;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
Db 21 FSRQYNFD 28

RESULT 7
US-09-270-767-61052
; Sequence 61052, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61052
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-61052

Query Match      78.9%; Score 30; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8
Db 30 KYNFD 34

RESULT 8
US-09-270-767-32252
; Sequence 32252, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32252
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32252

Query Match      78.9%; Score 30; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8
Db 132 KYNFD 136

RESULT 9
US-09-270-767-47469
; Sequence 47469, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
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; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47469
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-47469

Query Match      78.9%; Score 30; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8
Db 132 KYNFD 136

RESULT 10
US-09-270-767-34019
; Sequence 34019, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34019
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-34019

Query Match      78.9%; Score 30; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8
Db 103 KYNFD 107

RESULT 11
US-09-270-767-49236
; Sequence 49236, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49236
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-49236

Query Match      78.9%; Score 30; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 4 KYNFD 8  
|||||  
Db 103 KYNFD 107

## RESULT 12

US-09-526-597D-2  
; Sequence 2, Application US/09526597D  
; Patent No. 6710227  
; GENERAL INFORMATION:  
; APPLICANT: De Veylder, Lieven  
; APPLICANT: De Almeida, Janice  
; APPLICANT: Landrieu, Isabelle  
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof  
; FILE REFERENCE: 1187-2  
; CURRENT APPLICATION NUMBER: US/09/526,597D  
; CURRENT FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-526-597D-2

Query Match 78.9%; Score 30; DB 4; Length 209;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8  
|||||  
Db 186 KYNFD 190

## RESULT 13

US-09-328-352-7509  
; Sequence 7509, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 7509  
; LENGTH: 348  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-7509

Query Match 78.9%; Score 30; DB 4; Length 348;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8  
|||||  
Db 95 KYNFD 99

## RESULT 14

US-09-270-767-45543  
; Sequence 45543, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 45543  
; LENGTH: 363  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-45543

Query Match 78.9%; Score 30; DB 4; Length 363;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8  
|||||  
Db 283 KYNFD 287

## RESULT 15

US-09-140-466-2  
; Sequence 2, Application US/09140466  
; Patent No. 6288160  
; GENERAL INFORMATION:  
; APPLICANT: CLOUGH, BARBARA  
; APPLICANT: PREISER, PETER  
; APPLICANT: WILSON, ROBERT  
; TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE  
; TITLE OF INVENTION: MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS  
; TITLE OF INVENTION: EFFECTIVE AS ANTI-MALARIAL COMPOUNDS  
; FILE REFERENCE: N68837B GCW FJC DP  
; CURRENT APPLICATION NUMBER: US/09/140,466  
; CURRENT FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: US 60/056,246  
; EARLIER FILING DATE: 1997-08-28  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Plasmodium falciparum  
US-09-140-466-2

Query Match 78.9%; Score 30; DB 3; Length 410;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8  
|||||  
Db 160 KYNFD 164

Search completed: October 26, 2004, 15:34:19  
Job time : 14.2308 secs



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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 115.077 Seconds  
(without alignments)  
22.507 Million cell updates/sec

Title: US-09-574-735C-34

Perfect score: 38

Sequence: 1 FXXKYNFD 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	36	94.7	116	15	US-10-333-006-14	Sequence 14, Appl
2	36	94.7	221	15	US-10-425-114-69245	Sequence 69245, A
3	36	94.7	226	15	US-10-333-006-55	Sequence 55, Appl
4	36	94.7	256	11	US-09-993-308-2	Sequence 2, Appl
5	36	94.7	256	11	US-09-993-808B-2	Sequence 2, Appl
6	36	94.7	262	15	US-10-333-006-10	Sequence 10, Appl
7	36	94.7	263	15	US-10-425-114-63204	Sequence 63204, A
8	36	94.7	354	16	US-10-437-963-122432	Sequence 122432,
9	36	94.7	417	16	US-10-437-963-195115	Sequence 195115,
10	36	94.7	423	16	US-10-437-963-122443	Sequence 122443,
11	35	92.1	176	15	US-10-424-599-212181	Sequence 212181,
12	35	92.1	196	9	US-09-733-507-16	Sequence 16, Appl
13	35	92.1	196	15	US-10-451-139-15	Sequence 15, Appl

14	35	92.1	440	13	US-10-011-588-31	Sequence 31, Appl
15	35	92.1	441	13	US-10-011-588-11	Sequence 11, Appl
16	35	92.1	824	13	US-10-011-588-33	Sequence 33, Appl
17	35	92.1	1275	15	US-10-452-024-167	Sequence 167, App
18	35	92.1	1276	14	US-10-273-898-66	Sequence 66, Appl
19	35	92.1	1276	14	US-10-354-774-66	Sequence 66, Appl
20	35	92.1	1276	14	US-10-271-012-66	Sequence 66, Appl
21	35	92.1	1276	15	US-10-452-024-4	Sequence 4, Appl
22	35	92.1	1276	15	US-10-452-024-164	Sequence 164, App
23	35	92.1	1276	15	US-10-452-024-168	Sequence 168, App
24	35	92.1	1276	15	US-10-205-516-8	Sequence 8, Appl
25	35	92.1	1276	16	US-10-729-132-66	Sequence 66, Appl
26	35	92.1	1276	16	US-10-729-039-66	Sequence 66, Appl
27	35	92.1	1285	15	US-10-452-024-165	Sequence 165, App
28	35	92.1	1285	15	US-10-452-024-166	Sequence 166, App
29	35	92.1	1286	15	US-10-205-516-22	Sequence 22, Appl
30	35	92.1	1664	14	US-10-369-493-22428	Sequence 22428, A
31	34	89.5	90	15	US-10-333-006-13	Sequence 13, Appl
32	34	89.5	93	15	US-10-333-006-15	Sequence 15, Appl
33	34	89.5	137	9	US-09-733-507-14	Sequence 14, Appl
34	34	89.5	137	15	US-10-451-139-13	Sequence 13, Appl
35	34	89.5	190	9	US-09-993-308-4	Sequence 4, Appl
36	34	89.5	190	11	US-09-993-808B-4	Sequence 4, Appl
37	34	89.5	191	9	US-09-733-507-2	Sequence 2, Appl
38	34	89.5	191	9	US-09-733-507-10	Sequence 10, Appl
39	34	89.5	191	15	US-10-451-139-2	Sequence 2, Appl
40	34	89.5	194	15	US-10-333-006-44	Sequence 44, Appl
41	34	89.5	194	16	US-10-437-963-120870	Sequence 120870,
42	34	89.5	196	15	US-10-451-139-22	Sequence 22, Appl
43	34	89.5	205	15	US-10-424-599-235800	Sequence 235800,
44	34	89.5	212	9	US-09-733-507-12	Sequence 12, Appl
45	34	89.5	212	15	US-10-451-139-11	Sequence 11, Appl

#### ALIGNMENTS

RESULT 1  
US-10-333-006-14  
; Sequence 14, Application US/103333006  
; Publication No: US20040019926A1  
; GENERAL INFORMATION:  
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A111e S.  
; APPLICANT: Peres Bota, Adrian Marius  
; APPLICANT: Droual, Anne-Marie  
; APPLICANT: Mironov, Vladimir  
; APPLICANT: Inz, Dirk  
; APPLICANT: Hatzfeld, Yves  
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS  
; FILE REFERENCE: 1187-13  
; CURRENT APPLICATION NUMBER: US/10/333,006  
; CURRENT FILING DATE: 2003-01-14  
; PRIOR APPLICATION NUMBER: PCT/IB01/01492  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/218,471  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/241,219  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (11)-(11)  
; OTHER INFORMATION: Xaa = any amino acid  
US-10-333-006-14

Query Match 94.7%; Score 36; DB 15; Length 116;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
Db 89 FASKYNFD 96

RESULT 2  
US-10-425-114-69245  
; Sequence 69245, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313) B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 69245  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3079-036-F9\_FLI.pep  
US-10-425-114-69245

Query Match 94.7%; Score 36; DB 15; Length 221;  
Best Local Similarity 75.0%; Pred. No. 22;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
Db 193 FASKYNFD 200

RESULT 3  
US-10-333-006-55  
; Sequence 55, Application US/10333006  
; Publication No. US20040019926A1  
; GENERAL INFORMATION:  
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A1111 S.  
; APPLICANT: Peres Bota, Adrian Marius  
; APPLICANT: Droual, Anne-Marie  
; APPLICANT: Mironov, Vladimir  
; APPLICANT: Inz, Dirk  
; APPLICANT: Hatfield, Yves  
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS  
; FILE REFERENCE: 1167-13  
; CURRENT APPLICATION NUMBER: US/10/333,006  
; CURRENT FILING DATE: 2003-01-14  
; PRIOR APPLICATION NUMBER: PCT/IB01/01492  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/218,471  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/241,219  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 55  
; LENGTH: 226  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: probe or primer  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (119)..(119)  
; OTHER INFORMATION: Xaa = any amino acid

QY 1 FXXKYNFD 8  
Db 193 FASKYNFD 200

RESULT 3  
US-10-333-006-55  
; Sequence 55, Application US/10333006  
; Publication No. US20040019926A1  
; GENERAL INFORMATION:  
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A1111 S.  
; APPLICANT: Peres Bota, Adrian Marius  
; APPLICANT: Droual, Anne-Marie  
; APPLICANT: Mironov, Vladimir  
; APPLICANT: Inz, Dirk  
; APPLICANT: Hatfield, Yves  
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS  
; FILE REFERENCE: 1167-13  
; CURRENT APPLICATION NUMBER: US/10/333,006  
; CURRENT FILING DATE: 2003-01-14  
; PRIOR APPLICATION NUMBER: PCT/IB01/01492  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/218,471  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/241,219  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 55  
; LENGTH: 226  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: probe or primer  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (119)..(119)  
; OTHER INFORMATION: Xaa = any amino acid

US-10-333-006-55

Query Match 94.7%; Score 36; DB 15; Length 226;  
Best Local Similarity 75.0%; Pred. No. 23;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
Db 196 FASKYNFD 203

RESULT 4  
US-09-993-308-2  
; Sequence 2, Application US/09993308  
; Patent No. US20020159435A1  
; GENERAL INFORMATION:  
; APPLICANT: Gordon-Kamm, William J.  
; APPLICANT: Lowe, Keith S.  
; APPLICANT: Larkins, Brian A.  
; APPLICANT: Dilkes, Brian R.  
; APPLICANT: Sun, Yuejin  
; TITLE OF INVENTION: Cell Cycle Nucleic Acids, Polypeptides and Uses Thereof  
; FILE REFERENCE: 1146  
; CURRENT APPLICATION NUMBER: US/09/993,308  
; CURRENT FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: 60/246,349  
; PRIOR FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 2  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-09-993-308-2

Query Match 94.7%; Score 36; DB 9; Length 256;  
Best Local Similarity 75.0%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
Db 228 FASKYNFD 235

RESULT 5  
US-09-993-808B-2  
; Sequence 2, Application US/09993808B  
; Publication No. US20040003433A1  
; GENERAL INFORMATION:  
; APPLICANT: Gordon-Kamm, William  
; APPLICANT: Lowe, Keith  
; APPLICANT: Sun, Yuejin  
; APPLICANT: Dilkes, Brian  
; APPLICANT: Larkins, Brian  
; TITLE OF INVENTION: Cell Cycle Nucleic Acids, Polypeptides,  
; TITLE OF INVENTION: and Uses Thereof  
; FILE REFERENCE: 1146  
; CURRENT APPLICATION NUMBER: US/09/993,808B  
; CURRENT FILING DATE: 2001-11-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)..(256)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-993-808B-2

Query Match 94.7%; Score 36; DB 11; Length 256;  
Best Local Similarity 75.0%; Pred. No. 26;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
| | | | |  
Db 228 FASKYNFD 235

## RESULT 6

US-10-333-006-10  
; Sequence 10, Application US/10333006  
; Publication No. US20040019926A1  
; GENERAL INFORMATION:  
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A1111 S.  
; APPLICANT: Peres Bota, Adrian Marius  
; APPLICANT: Droual, Anne-Marie  
; APPLICANT: Mironov, Vladimir  
; APPLICANT: Inz, Dirk  
; APPLICANT: Hatze, Yves

; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS  
; FILE REFERENCE: 1187-13  
; CURRENT APPLICATION NUMBER: US/10/333,006  
; CURRENT FILING DATE: 2003-01-14  
; PRIOR APPLICATION NUMBER: PCT/IS01/01492  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/218,471  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/241,219  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 10  
; LENGTH: 262  
; TYPE: PRT  
; ORGANISM: Oryza sativa

US-10-333-006-10

Query Match 94.7%; Score 36; DB 15; Length 262;

Best Local Similarity 75.0%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
| | | | |  
Db 233 FASKYNFD 240

## RESULT 7

US-10-425-114-63204  
; Sequence 63204, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 63204  
; LENGTH: 263  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17355F05\_FLI.pep

US-10-425-114-63204

Query Match 94.7%; Score 36; DB 15; Length 263;

Best Local Similarity 75.0%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
| | | | |  
Db 235 FASKYNFD 242

## RESULT 8

US-10-437-963-122432  
; Sequence 122432, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 122432  
; LENGTH: 354  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_2535C.1.pep

US-10-437-963-122432

Query Match 94.7%; Score 36; DB 16; Length 354;

Best Local Similarity 75.0%; Pred. No. 35;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
| | | | |  
Db 219 FASKYNFD 226

## RESULT 9

US-10-437-963-195115  
; Sequence 195115, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 195115  
; LENGTH: 417  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_91095C.1.pep

US-10-437-963-195115

Query Match 94.7%; Score 36; DB 16; Length 417;

Best Local Similarity 75.0%; Pred. No. 42;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
Db 388 FAKYNFD 395

RESULT 10  
US-10-437-963-122443  
; Sequence 122443, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 122443  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_2536C.1.pep  
US-10-437-963-122443

Query Match 94.7%; Score 36; DB 16; Length 423;  
Best Local Similarity 75.0%; Pred. No. 42;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
Db 232 FAKYNFD 239

RESULT 11  
US-10-424-599-212181  
; Sequence 212181, Application US/10424599  
; Publication No. US20040301072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 212181  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_33625C.1.pep  
US-10-424-599-212181

Query Match 92.1%; Score 35; DB 15; Length 176;  
Best Local Similarity 75.0%; Pred. No. 28;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
Db 152 FTEKYNFD 159

RESULT 12  
US-09-733-507-16  
; Sequence 16, Application US/09733507  
; Patent No. US20010025379A1  
; GENERAL INFORMATION:  
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan  
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth  
; FILE OF INVENTION: Regulators  
; FILE REFERENCE: 81601-3  
; CURRENT APPLICATION NUMBER: US/09/733,507  
; CURRENT FILING DATE: 2000-12-02  
; PRIOR APPLICATION NUMBER: CA 2,256,121  
; PRIOR FILING DATE: 1998-12-31  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Chenopodium rubrum  
US-09-733-507-16

Query Match 92.1%; Score 35; DB 9; Length 196;  
Best Local Similarity 75.0%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
Db 171 FSEKYNFD 178

RESULT 13  
US-10-451-139-15  
; Sequence 15, Application US/10451139  
; Publication No. US20040098763A1  
; GENERAL INFORMATION:  
; APPLICANT: WANG, HONG  
; APPLICANT: ZHOU, YONGMING  
; APPLICANT: FOMKE, LAREY C.  
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF  
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA  
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR  
; FILE OF INVENTION: ACTIVITY  
; FILE REFERENCE: 4810-62237  
; CURRENT APPLICATION NUMBER: US/10/451,139  
; CURRENT FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/255,908  
; PRIOR FILING DATE: 2000-12-18  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Chenopodium rubrum  
US-10-451-139-15

Query Match 92.1%; Score 35; DB 15; Length 196;  
Best Local Similarity 75.0%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
Db 171 FSEKYNFD 178

RESULT 14  
US-10-011-588-31  
; Sequence 31, Application US/10011588  
; Publication No. US20020168727A1  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Leonard  
; APPLICANT: Jensen, Melody

;; TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM  
;; TITLE OF INVENTION: NEUROTOXINS AND LIGHT CHAIN FUSION PROTEINS FOR USE IN  
;; TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY  
;; FILE REFERENCE: A34796 067252.0113  
;; CURRENT APPLICATION NUMBER: US/10/011,588  
;; CURRENT FILING DATE: 2002-03-29  
;; PRIOR APPLICATION NUMBER: 09/910,186  
;; PRIOR FILING DATE: 2001-07-20  
;; PRIOR APPLICATION NUMBER: 09/611,419  
;; PRIOR FILING DATE: 2000-07-06  
;; PRIOR APPLICATION NUMBER: 60/246,744  
;; PRIOR FILING DATE: 2000-11-06  
;; PRIOR APPLICATION NUMBER: 60/311,966  
;; PRIOR FILING DATE: 2001-08-09  
;; NUMBER OF SEQ ID NOS: 47  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 31  
;; LENGTH: 440  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Recombinant protein encoded by SEQ ID NO:30  
US-10-011-588-31

Query Match 92.1%; Score 35; DB 13; Length 440;  
Best Local Similarity 75.0%; Pred. No. 69;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 FXXKYNFD 8  
| | | | |  
Db 324 FSEKYNFD 331

## RESULT 15

US-10-011-588-11  
;; Sequence 11, Application US/10011588  
;; Publication No. US20020168727A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Jensen, Melody  
;; TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM  
;; TITLE OF INVENTION: NEUROTOXINS AND LIGHT CHAIN FUSION PROTEINS FOR USE IN  
;; TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY  
;; FILE REFERENCE: A34796 067252.0113  
;; CURRENT APPLICATION NUMBER: US/10/011,588  
;; CURRENT FILING DATE: 2002-03-29  
;; PRIOR APPLICATION NUMBER: 09/910,186  
;; PRIOR FILING DATE: 2001-07-20  
;; PRIOR APPLICATION NUMBER: 09/611,419  
;; PRIOR FILING DATE: 2000-07-06  
;; PRIOR APPLICATION NUMBER: 60/246,744  
;; PRIOR FILING DATE: 2000-11-06  
;; PRIOR APPLICATION NUMBER: 60/311,966  
;; PRIOR FILING DATE: 2001-08-09  
;; NUMBER OF SEQ ID NOS: 47  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 11  
;; LENGTH: 441  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic botulinum neurotoxin light chain of  
;; OTHER INFORMATION: serotype D based on wild-type Clostridium  
;; OTHER INFORMATION: botulinum sequence  
US-10-011-588-11

Query Match 92.1%; Score 35; DB 13; Length 441;  
Best Local Similarity 75.0%; Pred. No. 69;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 FXXKYNFD 8  
| | | | |  
Db 325 FSEKYNFD 332

Search completed: October 26, 2004, 15:33:29  
Job time : 116.077 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:27:13 ; Search time 11.0769 Seconds  
(without alignments)  
69.490 Million cell updates/sec

Title: US-09-574-735C-34  
Perfect score: 38  
Sequence: 1 FXXKYNFD 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.79.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	92.1	196	2 T09968	cyclin-dependent k
2	35	92.1	627	2 D96956	ntrc family transc
3	35	92.1	1276	2 S11455	botulinum neurotox
4	35	92.1	1285	2 S70582	botulinum neurotox
5	35	92.1	1664	2 S72250	DNA-directed RNA p
6	34	89.5	191	2 T01132	cyclin-dependent k
7	34	89.5	699	2 A38368	chitinase (EC 3.2.
8	34	89.5	1635	2 T14075	chitinase (EC 3.2.
9	32	84.2	195	2 H36532	hypothetical prote
10	31	81.6	272	2 S71252	lectin-like protei
11	31	81.6	374	2 T10349	very-late factor 1
12	31	81.6	480	2 T08866	hypothetical prote
13	31	81.6	603	2 G84554	probable acyl-CoA
14	31	81.6	648	2 S97733	transcription acti
15	31	81.6	814	1 C40618	fimbrial outer mem
16	31	81.6	838	2 AC1064	outer membrane fim
17	31	81.6	1050	2 H93316	hypothetical prote
18	30	78.9	114	2 AC3246	hypothetical prote
19	30	78.9	149	2 A70325	hypothetical prote
20	30	78.9	209	2 T46140	hypothetical prote
21	30	78.9	232	2 F84576	hypothetical prote
22	30	78.9	251	2 T40710	hypothetical prote
23	30	78.9	260	2 D64419	hypothetical prote
24	30	78.9	265	2 T29973	hypothetical prote
25	30	78.9	286	2 B90546	hypothetical prote
26	30	78.9	302	2 B84979	sulfate adenylyltr
27	30	78.9	315	2 H84938	flagellar motor sw
28	30	78.9	321	2 AB1316	heptaprenyl diphos
29	30	78.9	321	2 AB1688	heptaprenyl diphos

30 30 78.9 330 2 C71180 probable N-acetyl-D-2-hydroxy-acid d  
31 30 78.9 331 2 F64047 probable exported  
32 30 78.9 334 2 A10284 hypothetical prote  
33 30 78.9 345 2 T33906 hypothetical prote  
34 30 78.9 365 2 E30039 secretory protein  
35 30 78.9 399 2 S27879 hypothetical prote  
36 30 78.9 408 2 T18813 hypothetical prote  
37 30 78.9 410 1 I40755 trigger factor 2 (translation elonga  
38 30 78.9 410 2 S72277 hypothetical prote  
39 30 78.9 413 2 A82163 trigger factor tig  
40 30 78.9 444 2 H81437 xylulokinase homol  
41 30 78.9 487 2 E89895 phenylalanine-tRNA  
42 30 78.9 552 2 T28732 probable solute-bi  
43 30 78.9 609 2 H83419 hypothetical prote  
44 30 78.9 617 2 H84957 NADH2 dehydrogenas  
45 30 78.9 644 2 S44478

ALIGNMENTS

RESULT 1

T09968 cyclin-dependent kinase inhibitor protein - red goosefoot

C:Species: Chenopodium rubrum (red goosefoot)

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: T09968

R:Fontain, M.D.; Renz, A.; Beck, E.

A:Description: A plant G1 cyclin-dependent kinase inhibitor gene from a photoautotroph.

A:Reference number: Z16910

A:Accession: T09968

A>Status: Preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-136 <FOU>

A:Cross-references: UNIPROT:O48597; EMBL:AJ002173

A:Experimental source: photoautotrophic cells derived from hypocotyl tissue

C:Genetics:

A:Gene: CDK11

C:Keywords: protein kinase inhibitor

Query Match 92.1%; Score 35; DB 2; Length 196;

Best Local Similarity 75.0%; Pred. No. 4;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8

DB 171 FSEKYNFD 178

RESULT 2

D96956 ntrc family transcription regulator (PAS and AAA domains) [imported] - Clostridium acet

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004

C:Accession: D96956

R:Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: D96956

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-627 <XUR>

A:Cross-references: UNIPROT:Q97LU5; GB:AE001437; PIDN:AAK78439.1; PID:G15023316; GSPDB:

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC0459

Query Match 92.1%; Score 35; DB 2; Length 627;

Best Local Similarity 75.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;





Query Match 89.5%; Score 34; DB 2; Length 191;  
Best Local Similarity 75.0%; Pred. No. 6.4; Mismatches 0; Gaps 0;  
Matches 6; Conservative 0; Indels 2;

QY 1 FXXKYNFD 8  
| | | | |  
Db 167 FKKYNFD 174

RESULT 7  
A38368  
chitinase (EC 3.2.1.14) precursor - Bacillus circulans  
C:Species: Bacillus circulans  
C:Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 09-Jul-2004  
C:Accession: A38368  
R;Matanabe, T.; Suzuki, K.; Oyanagi, W.; Ohnishi, K.; Tanaka, H.  
J. Biol. Chem. 265, 15659-15665, 1990  
A:Title: Gene cloning of chitinase A1 from Bacillus circulans WL-12 revealed its evolution  
A:Reference number: A38368; MUID:90368776; PMID:2203782  
A:Accession: A38368  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-699 <WAT>  
A:Cross-references: UNIPROT:P20533; GB:M57601; GB:J05599; NID:G1066341; PIDN:AAA81528.1;  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 89.5%; Score 34; DB 2; Length 699;  
Best Local Similarity 75.0%; Pred. No. 24; Mismatches 0; Gaps 0;  
Matches 6; Conservative 0; Indels 2;

QY 1 FXXKYNFD 8  
| | | | |  
Db 190 FLKYNFD 197

RESULT 8  
T14075  
chitinase (EC 3.2.1.14) - yellow fever mosquito  
C:Species: Aedes aegypti (yellow fever mosquito)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T14075  
R;de la Vega, H.; Specht, C.A.; Liu, Y.; Robbins, P.W.  
Insect Mol. Biol. 7, 233-239, 1997  
A:Title: Chitinases are a multi-gene family in Aedes, Anopheles, and Drosophila.  
A:Reference number: Z17872  
A:Accession: T14075  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1635 <DEL>  
A:Cross-references: UNIPROT:O17412; EMBL:AF026492; NID:G2564720; PID:G2564721; PIDN:AA8B  
C:Genetics:  
A:Gene: CHT2  
A:Introns: 462/3; 524/3; 618/1; 951/3; 1151/2  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 89.5%; Score 34; DB 2; Length 1635;  
Best Local Similarity 75.0%; Pred. No. 58; Mismatches 0; Gaps 0;  
Matches 6; Conservative 0; Indels 2;

QY 1 FXXKYNFD 8  
| | | | |  
Db 1365 FIEKYNFD 1372

RESULT 9  
H96532  
hypothetical protein F14J22.14 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: H96532  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: H96532  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-195 <STO>  
A:Cross-references: UNIPROT:Q9FX90; GB:AE005173; NID:G10120423; PIDN:AAG13048.1; GSPDB:  
C:Genetics:  
A:Gene: F14J22.14  
A:Map position: 1

Query Match 84.2%; Score 32; DB 2; Length 195;  
Best Local Similarity 62.5%; Pred. No. 17; Mismatches 1; Indels 2; Gaps 0;  
Matches 5; Conservative 1;

QY 1 FXXKYNFD 8  
| | | | |  
Db 170 FTEKYNFD 177

RESULT 10  
S71252  
lectin-like protein - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 28-Oct-1996 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C:Accession: S71252  
R;Herve, C.; Lescure, B.  
submitted to the EMBL Data Library, September 1995  
A:Description: An Arabidopsis thaliana cDNA encoding a lectin like protein.  
A:Reference number: S71252  
A:Accession: S71252  
A:Molecule type: mRNA  
A:Residues: 1-272 <HER>  
A:Cross-references: UNIPROT:Q39205; EMBL:X91259; NID:G995618; PID:G995619  
C:Superfamily: plant lectin  
C:Keywords: lectin

Query Match 81.6%; Score 31; DB 2; Length 272;  
Best Local Similarity 62.5%; Pred. No. 39; Mismatches 1; Indels 2; Gaps 0;  
Matches 5; Conservative 1;

QY 1 FXXKYNFD 8  
| | | | |  
Db 18 FAVKFNFD 25

RESULT 11  
T10349  
very-late factor 1 protein - Orgyia pseudotsugata nuclear polyhedrosis virus  
C:Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OPMNV  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
C:Accession: T10349  
R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.  
Virology 229, 381-399, 1997  
A:Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis  
A:Reference number: Z17011; MUID:97271300; PMID:9126251  
A:Accession: T10349  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-374 <HR>  
A:Cross-references: EMBL:U75930; NID:G2934903; PIDN:AAC59079.1; PID:G1911326

Query Match 81.6%; Score 31; DB 2; Length 374;  
Best Local Similarity 62.5%; Pred. No. 54; Mismatches 1; Indels 2; Gaps 0;  
Matches 5; Conservative 1;

QY 1 FXXKYNFD 8  
 Db 335 YLKNYFD 342

## RESULT 12

T08866  
 hypothetical protein A.TM017A05.12 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
 C:Accession: T08866

R:Waterston, R.  
 submitted to the EMBL Data Library, October 1997  
 A:Reference number: Z16500  
 A:Accession: T08866  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-480 <WAT>  
 A:Cross-references: UNIPROT:Q9SEY5; EMBL:AF024504; NID:G2435510; PID:G2435522; GSPDB:GNQ  
 A:Experimental source: cultivar Columbia  
 C:Genetics:  
 A:Gene: ATSP:A.TM017A05.12  
 A:Map position: 4  
 C:Superfamily: probable acyl-CoA ligase medium chain; acetate-CoA ligase homology  
 F:7-7/470/Domain: acetate-CoA ligase homology <ACL>

Query Match 81.6%; Score 31; DB 2; Length 480;  
 Best Local Similarity 62.5%; Pred. No. 70;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
 Db 88 FASKYSFD 95

## RESULT 13

G84554  
 Probable acyl-CoA synthetase [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
 C:Accession: G84554

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; MUID:20083487; PMID:10617197  
 A:Accession: G84554  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-603 <STO>  
 A:Cross-references: UNIPROT:Q9SEY5; GB:AE002093; NID:G6598797; PIDN:AAF18674.1; GSPDB:GN  
 C:Genetics:  
 A:Gene: At2g17650  
 A:Map position: 2  
 C:Superfamily: probable acyl-CoA ligase medium chain; acetate-CoA ligase homology

Query Match 81.6%; Score 31; DB 2; Length 603;  
 Best Local Similarity 62.5%; Pred. No. 89;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
 Db 211 FASKYSFD 218

## RESULT 14

S59723  
 transcription activator CHA4 - yeast (Saccharomyces cerevisiae)  
 N/Alternate names: protein L2552; protein YLR098C  
 C:Species: Saccharomyces cerevisiae  
 C:Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 16-Aug-2004  
 C:Accession: S59723; S64932; S72236

R:Schjerling, P.  
 submitted to the EMBL Data Library, June 1995  
 A:Reference number: S59723  
 A:Accession: S59723  
 A:Molecule type: DNA  
 A:Residues: 1-648 <SCH>  
 A:Cross-references: UNIPROT:P43634; EMBL:Z49975; NID:G9886706; PIDN:CAA90276.1; PID:G98867  
 R:Benes, V.; Rechmann, S.; Nentwich, U.; Schwager, C.; Ansoerge, W.; Vosse, H.  
 submitted to the Protein Sequence Database, May 1996

A:Reference number: S64920  
 A:Accession: S64932  
 A:Molecule type: DNA  
 A:Residues: 1-648 <BEN>  
 A:Cross-references: EMBL:Z73270; NID:G1360478; PIDN:CAA97662.1; PID:e245801; PID:G136047  
 R:Holmberg, S.; Schjerling, P.  
 Genetics 144, 467-478, 1996

A:Title: Cha4p of Saccharomyces cerevisiae activates transcription via serine/threonine  
 A:Reference number: S72236; MUID:97044442; PMID:8889513  
 A:Accession: S72236

A:Molecule type: DNA  
 A:Residues: 1-648 <HOL>  
 A:Cross-references: EMBL:Z49975; NID:G9886706; PIDN:CAA90276.1; PID:G9886707  
 C:Genetics:  
 A:Gene: SGD:CHA4  
 A:Map position: 12R  
 A:Cross-references: SGD:S0004088; MIPS:YLR098C

C:Function:  
 A:Description: activation of CHA1; binds to UAS1(CHA) and UAS2(CHA) elements in CHA1 pro  
 C:Superfamily: GAL4 zinc binuclear cluster homology  
 C:Keywords: DNA binding; nucleus  
 F:39-75/Domain: GAL4 zinc binuclear cluster homology <GAL4>

Query Match 81.6%; Score 31; DB 2; Length 648;  
 Best Local Similarity 62.5%; Pred. No. 96;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
 Db 620 FALEYNFD 627

## RESULT 15

C40618  
 fimbrial outer membrane protein homolog sefc - Salmonella enteritidis  
 C:Species: Salmonella enteritidis  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C:Accession: C40618  
 R:Clouthier, S.C.; Muller, K.H.; Doran, J.L.; Collinson, S.K.; Kay, W.W.  
 J. Bacteriol. 175, 2523-2533, 1993

A:Title: Characterization of three fimbrial genes, sefABC, of Salmonella enteritidis.  
 A:Reference number: A40618; MUID:93239677; PMID:8097515  
 A:Contents: 27655-3b  
 A:Accession: C40618  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-814 <CLO>  
 A:Cross-references: UNIPROT:P33388; GB:L11010; NID:G310649; PIDN:AAA27221.1; PID:G310650  
 A:Note: sequence extracted from NCBI backbone (NCBIN:130387, NCBIP:130397)  
 C:Superfamily: outer membrane usher protein fimD  
 C:Keywords: membrane protein

Query Match 81.6%; Score 31; DB 1; Length 814;  
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
 Db 21 FSRQYNFD 28

Search completed: October 26, 2004, 15:40:06  
 Job time : 14.0769 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:27:03 ; Search time 44.6154 Seconds  
(without alignments)  
103.171 Million cell updates/sec

Title: US-09-574-735C-34  
Perfect score: 38  
Sequence: 1 FXXKYNFD 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	36	94.7	262	2	Q6Z6G5	Q6Z6G5 oryza sativ
2	36	94.7	262	2	BAD17213	BAD17213 oryza sat
3	35	92.1	113	2	O17419	O17419 anopheles s
4	35	92.1	196	2	O48597	O48597 nicotiana t
5	35	92.1	207	2	O8GUA2	O8GUA2 nicotiana t
6	35	92.1	442	2	Q8EV36	Q8EV36 mycoplasma
7	35	92.1	627	2	Q97LU5	Q97LU5 clostridium
8	35	92.1	1275	2	Q9QTG7	Q9QTG7 clostridium
9	35	92.1	1276	1	EXD_CLOBO	P19321 clostridium
10	35	92.1	1285	2	Q45967	Q45967 clostridium
11	35	92.1	1285	2	Q9LBR1	Q9LBR1 clostridium
12	35	92.1	1640	2	O759A3	O759A3 ashbya goss
13	35	92.1	1640	2	AA552294	AA552294 ashbya go
14	35	92.1	1643	2	Q6FV16	Q6FV16 candida gla
15	35	92.1	1653	2	Q6CIX4	Q6CIX4 kluyveromyc
16	35	92.1	1664	1	RPAL_YEAST	P10964 saccharomyc
17	34	89.5	113	2	O17414	O17414 anopheles g
18	34	89.5	156	2	Q93YF6	Q93YF6 nicotiana t
19	34	89.5	163	2	Q93Y92	Q93Y92 nicotiana t
20	34	89.5	185	2	Q8GT28	Q8GT28 lycopersico
21	34	89.5	189	2	Q9LRY0	Q9LRY0 arabidopsis
22	34	89.5	191	2	O04154	O04154 arabidopsis
23	34	89.5	191	2	O82809	O82809 arabidopsis
24	34	89.5	191	2	O8LDX1	O8LDX1 arabidopsis
25	34	89.5	196	2	O9LJL5	O9LJL5 arabidopsis
26	34	89.5	210	2	Q8GT29	Q8GT29 lycopersico
27	34	89.5	222	2	Q9FKB5	Q9FKB5 arabidopsis
28	34	89.5	242	2	Q7XDH8	Q7XDH8 oryza sativ
29	34	89.5	242	2	Q9FW65	Q9FW65 oryza sativ
30	34	89.5	286	2	Q8GYJ3	Q8GYJ3 arabidopsis
31	34	89.5	286	2	Q94CM0	Q94CM0 arabidopsis

32 34 89.5 289 2 O48846 O48846 arabidopsis  
33 34 89.5 474 2 O86LZ2 O86LZ2 lutzomyia l  
34 34 89.5 484 2 Q9W092 Q9W092 grosophila  
35 34 89.5 553 2 Q704Y2 Q704Y2 lacanobia o  
36 34 89.5 553 2 CAF05663 CAF05663 lacanobia o  
37 34 89.5 557 2 Q8WTK0 Q8WTK0 chorisoneu  
38 34 89.5 699 1 CH11\_BACCI P20533 bacillus ci  
39 34 89.5 699 2 O48494 O48494 kurthia zop  
40 34 89.5 717 2 O9KHB3 O9KHB3 bacillus ci  
41 34 89.5 1037 2 O8VLO3 O8VLO3 alteromonas  
42 34 89.5 1322 2 Q6CKZ5 Q6CKZ5 kluyveromyc  
43 34 89.5 1635 2 O17412 O17412 aedes aegypt  
44 32 84.2 166 2 Q6T220 Q6T220 glycine max  
45 32 84.2 166 2 AAS13377 AAS13377 glycine m

ALIGNMENTS

RESULT 1

Q6Z6G5 PRELIMINARY; PRT; 262 AA.

AC Q6Z6G5;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein P0486G03.18.  
GN Name=P0486G03.18;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP005002; BAD17213.1; -  
DR InterPro; IPR003175; CDI.  
DR Pfam; PF02234; CDI; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 262 AA; 27138 MW; 42EC85C8276C0726 CRC64;

Query Match 94.7%; Score 36; DB 2; Length 262;  
Best Local Similarity 75.0%; Pred. No. 24;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8

DB 233 FAKYNFD 240

RESULT 2

BAD17213 PRELIMINARY; PRT; 262 AA.

AC BAD17213;  
DT 10-MAY-2004 (TrEMBLrel. 27, Created)  
DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein P0486G03.18.  
GN P0486G03.18.  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=cv. Nipponbare;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RL "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, PAC clone:P0486G03.18";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP005002; BAD17213.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 262 AA; 27138 MW; 42EC85C8276C0726 CRC64;

Query Match 94.7%; Score 36; DB 2; Length 262;  
Best Local Similarity 75.0%; Pred. No. 24;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
| | | | |  
DB 233 FAKYNFD 240

## RESULT 3

Q17419 PRELIMINARY; PRT; 113 AA.  
AC O17419;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Chitinase (Fragment).  
GN Name=Chit3;  
OS Anopheles stephensi (Indo-Pakistan malaria mosquito).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.  
OX NCBI\_TaxID=30069;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98324849; PubMed=9662472;  
RA de la Vega H., Specht C.A., Liu Y., Robbins P.W.;  
RT "Chitinases are a multi-gene family in Aedes, Anopheles and  
RT Drosophila."  
RL Insect Mol. Biol. 7:233-239(1998).  
DR EMBL; AF026499; AAB81897.1; -;  
DR HSP; Q13231; ILG2.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR InterPro; IPR001223; P:metabolism; IEA.  
DR InterPro; IPR001579; Glyco\_hydro\_18.  
DR Pfam; PF00704; Glyco\_hydro\_18; 1-18AS.  
DR PROSITE; PS01095; CHITINASE\_18; PARTIAL.  
FT NON\_TER 1  
FT NON\_TER 113  
SQ SEQUENCE 113 AA; 13188 MW; 5EA7DCA6B54B4B37 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 113;  
Best Local Similarity 75.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
| | | | |  
DB 100 FAKYNFD 107

## RESULT 4

O48597 PRELIMINARY; PRT; 196 AA.  
AC O48597;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cyclin-dependent kinase inhibitor protein.  
GN Name=CDK1;  
OS Chenopodium rubrum (Red goosefoot) (pigweed).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Amaranthaceae; Chenopodium.  
OX NCBI\_TaxID=3560;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99329903; PubMed=10409053;  
RA Fountain M.D., Renz A., Beck E.;  
RT "Isolation of a cDNA encoding a G1-cyclin-dependent kinase inhibitor

RT from suspension-cultured photoautotrophic chenopodium rubrum cells.";  
RL Plant Physiol. 120:339-339(1999).  
DR EMBL; AJ002173; CAA05215.1; -;  
DR PIR; T09968; T09968.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a.; IEA.  
DR GO; GO:0016301; F:kinase activity; IEA.  
DR GO; GO:0007050; P:cell cycle arrest; IEA.  
DR InterPro; IPR003175; CDI.  
DR Pfam; PF02234; CDI; 1.  
KW Cyclin; Kinase.  
SQ SEQUENCE 196 AA; 21685 MW; 150349F7ED82A6B2 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 196;  
Best Local Similarity 75.0%; Pred. No. 29;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
| | | | |  
DB 171 FSEKYNFD 178

## RESULT 5

Q8GUA2 PRELIMINARY; PRT; 207 AA.  
AC Q8GUA2;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cyclin-dependent kinase inhibitor.  
GN Name=Kis2;  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Jasinski S., Sardaiva Leite C., Domenichini S., Stevens R., Raynaud C.,  
RA Perennes C., Bergounioux C., Glab N.;  
RT "Ntkis2, a novel tobacco cyclin-dependent kinase inhibitor  
RT differentially expressed during the cell cycle and plant  
RT development."  
RL Plant Physiol. Biochem. 41:667-676(2003).  
DR EMBL; AJ517183; CAD56868.1; -;  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a.; IEA.  
DR GO; GO:0016301; F:kinase activity; IEA.  
DR GO; GO:0007050; P:cell cycle arrest; IEA.  
DR InterPro; IPR003175; CDI.  
DR Pfam; PF02234; CDI; 1.  
KW Cyclin; Kinase.  
SQ SEQUENCE 207 AA; 23278 MW; F5AE70AD2261BC2D CRC64;

## Query Match

Best Local Similarity 92.1%; Score 35; DB 2; Length 207;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
| | | | |  
DB 180 FTKYNFD 187

## RESULT 6

Q8EV36 PRELIMINARY; PRT; 442 AA.  
AC Q8EV36;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Conserved hypothetical.  
GN OrderedLocusNames=NYPE7310;  
OS Mycoplasma penetrans.

```

DR PROSITE; PS00676; SIGMA54_INTERACT_2; 1.
DR PROSITE; PS50045; SIGMA54_INTERACT_4; 1.
KW ATP-binding; Complete proteome; DNA-binding; Transcription regulation.
SQ SEQUENCE 627 AA; 71082 MW; 4A652FA3AB362AD0 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 627;
Best Local Similarity 75.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXXYNFD 8
DB 311 FVAKYNFD 318
|||||

RESULT 8
Q9QTG7 PRELIMINARY; PRT; 1275 AA.
ID Q9QTG7
AC Q9QTG7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE NTX (Fragment).
GN Name=ntx;
OS Clostridium botulinum D bacteriophage.
OC Viruses.
OC NCBI_TaxID=29342;
OX [1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=1873;
RX MEDLINE=99017546; PubMed=9802560;
RA Nakajima H., Inoue K., Ikeda T., Fujinaga Y., Sunagawa H., Takeshi K., Ohya Y., Watanabe T., Inoue K., Oguma K.;
RT "Molecular composition of the 16S toxin produced by a Clostridium botulinum type D strain, 1873."
RL Microbiol. Immunol. 42:599-605(1998).
DR EMBL; AB012112; BAAV5084.1; -
DR GO; GO:0008233; F:Peptidase activity; IEA.
DR GO; GO:0009405; P:Pathogenesis; IEA.
DR GO; GO:0006508; P:Proteolysis and peptidolysis; IEA.
DR InterPro; IPRO11591; Botulinum.
DR InterPro; IPRO08985; ConA like lec_g1.
DR InterPro; IPRO11065; Kunitz like.
DR InterPro; IPRO00395; Peptidase M27.
DR InterPro; IPRO06025; Peptidase M27.
DR Pfam; PF01742; Peptidase M27; 1.
DR PRINTS; PR00760; BONTOKILYSIN.
DR ProDom; PD001963; Botulinum; 1.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN_1.
FT NON_TER 1275 1275
SQ SEQUENCE 1275 AA; 146742 MW; 3C50F46C6233E2D6 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 1275;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXXYNFD 8
DB 326 FSEXYNFD 333
|||||

RESULT 9
BXD_CLOBO
ID BXD_CLOBO STANDARD; PRT; 1276 AA.
AC P19321;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Botulinum neurotoxin type D precursor (EC 3.4.24.69) (BONT/D)
GN Name=botD;
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.

```

DR	InterPro:	IPR006025;	Pept_M_Zn_BS.
DR	Pfam:	PF01742;	Peptidase M27; 1.
DR	PRINTS:	PR00760;	BONTOXILYSIN.
DR	ProDom:	PD001963;	Bontokilysin; 1.
DR	PROSITE:	PS00142;	ZINC_PROTEASE; 1.
KW	Direct protein sequencing;	Hydrolase; Metalloprotease; Neurotoxin;	
KW	Transmembrane; Zinc.		
FT	CHAIN	1	442
FT	CHAIN	443	1276
FT	METAL	229	229
FT	ACT_SITE	230	230
FT	METAL	233	233
FT	DISULFID	437	450
FT	VARIANT	15	16
FT	VARIANT	17	18
FT	VARIANT	452	452
FT	VARIANT	457	457
FT	VARIANT	457	457
FT	VARIANT	462	462
FT	VARIANT	489	489
FT	VARIANT	644	644
FT	VARIANT	1122	1122
SQ	SEQUENCE	1276 AA;	146871 MW; CIECSOF46C6233E2 CRC64;
Query Match			
Best Local Similarity 92.1%; Score 35; DB 1; Length 1276;			
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps			
Qy	1	FXXKYNFD 8	
Dd	326	FSEKYNFD 333	
RESULT 10			
Q45967			
ID	Q45967	PRELIMINARY;	PRT; 1285 AA.
AC	Q45967;		
DT	01-NOV-1996	(TrEMBLrel.. 01, Created)	
DD	01-NOV-1996	(TrEMBLrel.. 01, Last sequence update)	
DT	01-MAR-2004	(TrEMBLrel.. 26, Last annotation update)	
DE	Neurotoxin consisting of botulinum neurotoxin D and Cl.		
OS	Clostridium botulinum D.		
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;		
CC	Clostridium.		
NCBI_TaxID=36829;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-South African;		
RX	MEDLINE=96283801; PubMed=8679691;		
RA	Moriishi K., Koura M., Abe N., Fujii N., Fujinaga Y., Inoue K., Oguma K.;		
RT	"Mosaic structures of neurotoxins produced from Clostridium botulinum types C and D organisms."		
RL	Biochim. Biophys. Acta 1307:123-126(1996).		
DR	EMBL; D38442; EAA07477.1; -.		
DR	HSPF; P10844; IF31.		
DR	MEROPS; M27.002; -.		
DR	GO; GO:0008233; P:peptidase activity; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR011591; Botulinum.		
DR	InterPro; IPR008985; CoxA-like lec_gl.		
DR	InterPro; IPR011085; Kunitz-like.		
DR	InterPro; IPR000395; Peptidase M27.		
DR	InterPro; IPR006025; Pept_M_Zn_BS.		
DR	Pfam; PF01742; Peptidase M27; 1.		
DR	PRINTS; PR00760; BONTOXILYSIN.		
DR	ProDom; PD001963; Botulinum; 1.		
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.		
KW	NEUROTOXIN.		
SQ	SEQUENCE	1285 AA;	147365 MW; EEDE98E43CAC413 CRC64;
Query Match			
92.1%; Score 35; DB 2; Length 1285;			



Best Local Similarity 75.0%; Pred. No. 2e+02; Mismatches 0; Indels 2; Gaps 0;  
Matches 6; Conservative 0;

QY 1 FXXKYNFD 8  
| | | | |  
Db 326 FSEKYNFD 333

## RESULT 11

ID Q9LBR1 PRELIMINARY; PRT; 1285 AA.  
AC Q9LBR1;  
DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Neurotoxin.  
OS Clostridium botulinum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1491;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D-4947;  
RA MEDLINE=21659747; PubMed=11713244;  
RX Kouguchi H., Watanabe T., Sagane Y., Sunagawa H., Ohyama T.;  
RT "in vitro reconstruction of the clostridium botulinum type D  
progenitor toxin."  
RL J. Biol. Chem. 277:2650-2656(2002).  
DR EMBL; AB037920; BAA90661.1; --  
DR HSRF; P10844; I131.  
DR MEROPS; M27.002; --  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPRO11591; Botulinum.  
DR InterPro; IPRO08965; ConA like lec\_gl.  
DR InterPro; IPRO11065; Kunitz\_like.  
DR InterPro; IPRO00395; Peptidase\_M27.  
DR InterPro; IPRO06025; Pept M Zn\_BS.  
DR Pfam; PF01742; Peptidase\_M27; 1.  
DR PRINTS; PR00760; BONTOXILysin.  
DR ProDom; PD001963; Botulinum; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Neurotoxin.  
SQ SEQUENCE 1285 AA; 147351 MW; B63AFA487D570680 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 1285;  
Best Local Similarity 75.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
| | | | |  
Db 326 FSEKYNFD 333

## RESULT 12

ID Q759A3 PRELIMINARY; PRT; 1640 AA.  
AC Q759A3;  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE ADR374Cp.  
GN Name=ADR374C;  
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.  
OX NCBI\_TaxID=33169;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 10895;  
RX PubMed=15001715;  
RA Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,

RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavner A.,  
RA Gaffney T.D., Philippsen P.;  
RT "The Ashbya gossypii genome as a tool for mapping the ancient  
RT Saccharomyces cerevisiae genome."  
RL Science 304:304-307(2004).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 10895;  
RA Voegeli S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,  
RA Philippsen P.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB016893; AAS52294.1; --  
DR AGD; ADR374C; --

DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR006592; RNA\_pola\_N.  
DR InterPro; IPR000722; RNA\_pol\_A.  
DR InterPro; IPR007080; RNA\_pol\_Rpb1\_1.  
DR InterPro; IPR007066; RNA\_pol\_Rpb1\_3.  
DR InterPro; IPR007083; RNA\_pol\_Rpb1\_4.  
DR InterPro; IPR007081; RNA\_pol\_Rpb1\_5.  
DR Pfam; PF04997; RNA\_pol\_Rpb1\_1; 1.  
DR Pfam; PF00623; RNA\_pol\_Rpb1\_2; 1.  
DR Pfam; PF04983; RNA\_pol\_Rpb1\_3; 1.  
DR Pfam; PF05000; RNA\_pol\_Rpb1\_4; 1.  
DR Pfam; PF04998; RNA\_pol\_Rpb1\_5; 1.  
DR SMART; SM00663; RPOLA\_N; 1.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
SQ SEQUENCE 1640 AA; 182887 MW; 4B89F52FC18BCDF0 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 1640;  
Best Local Similarity 75.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
| | | | |  
Db 1432 FISKYNFD 1439

## RESULT 13

ID AAS52294 PRELIMINARY; PRT; 1640 AA.  
AC AAS52294;  
DT 23-APR-2004 (TRENBLrel. 27, Created)  
DT 23-APR-2004 (TRENBLrel. 27, Last sequence update)  
DT 23-APR-2004 (TRENBLrel. 27, Last annotation update)  
DE ADR374Cp.  
GN ADR374C.  
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.  
OX NCBI\_TaxID=33169;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 10895;  
RX PubMed=15001715;  
RA Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,  
RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavner A.,  
RA Gaffney T.D., Philippsen P.;  
RT "The Ashbya gossypii genome as a tool for mapping the ancient  
RT Saccharomyces cerevisiae genome."  
RL Science 304:304-307(2004).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 10895;  
RA Voegeli S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,  
RA Philippsen P.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB016893; AAS52294.1; --  
DR EMBL; ADR374C; 182887 MW; 4B89F52FC18BCDF0 CRC64;  
SQ SEQUENCE 1640 AA; 182887 MW; 4B89F52FC18BCDF0 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 1640;  
Best Local Similarity 75.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
| | | | |  
Db 326 FSEKYNFD 333

QY 1 FXXKYNFD 8  
Db 1432 FISKYNFD 1439

RESULT 14  
Q6FV16 PRELIMINARY; PRT; 1643 AA.  
AC Q6FV16;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Strain CBS138 chromosome E complete sequence.  
GN ORFNames=CAGLOE05500g;  
OS Candida glabrata (Yeast) (Torulopsis glabrata).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=5478;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CBS138;  
RG GENOLEVURES;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
RA Boisarame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
RA Swennene D., Tekaja F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.L.;  
RT "Genome evolution in yeasts."  
RL Nature 430:35-44(2004).  
DR EMBL; CR380951; CAG58847.1; -  
DR InterPro; IPR000345; CytC heme BS.  
DR InterPro; IPR006592; RNA polA N.  
DR InterPro; IPR000722; RNA pol A.  
DR InterPro; IPR007080; RNA pol Rpb1 1.  
DR InterPro; IPR007066; RNA pol Rpb1 3.  
DR InterPro; IPR007083; RNA pol Rpb1 4.  
DR InterPro; IPR007081; RNA pol Rpb1 5.  
DR Pfam; PF04997; RNA pol Rpb1 1; 1.  
DR Pfam; PF00623; RNA pol Rpb1 2; 1.  
DR Pfam; PF04983; RNA pol Rpb1 3; 1.  
DR Pfam; PF05000; RNA pol Rpb1 4; 1.  
DR Pfam; PF04998; RNA pol Rpb1 5; 1.  
DR SMART; SMO0663; RPOLA N; 1.  
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.  
SQ SEQUENCE 1643 AA; 184865 MW; FD2B3ED14021FC18 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 1643;  
Best Local Similarity 75.0%; Pred.No. 2.5e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
Db 1437 FVTKYNFD 1444

RESULT 15  
Q6CIX4 PRELIMINARY; PRT; 1653 AA.  
AC Q6CIX4;  
DT 01-OCT-2004 (TrEMBLrel. 28, Created)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Strain NRRL Y-1140 chromosome F of strain NRRL Y-1140 of Kluyveromyces

DE lactis.  
GN ORFNames=KLLA0F23243g;  
OS Kluyveromyces lactis (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
OX NCBI\_TaxID=28985;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NRRL Y-1140;  
RG GENOLEVURES;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
RA Boisarame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
RA Swennene D., Tekaja F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.L.;  
RT "Genome evolution in yeasts."  
RL Nature 430:35-44(2004).  
DR EMBL; CR382126; CAG98823.1; -  
DR EMBL; CR382126; CAG98823.1; -  
SQ SEQUENCE 1653 AA; 185832 MW; E1A9732C0AAE8387 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 1653;  
Best Local Similarity 75.0%; Pred.No. 2.5e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8  
Db 1447 FVTKYNFD 1454

Search completed: October 26, 2004, 15:39:25  
Job time : 48.6154 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 44.6154 Seconds  
(without alignments)  
64.324 Million cell updates/sec

Title: US-09-574-735C-35

Perfect score: 40

Sequence: 1 XLXGRYEW 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	95.0	8	5	ABG65714 Plant ICK
2	38	95.0	53	5	ABG65677 Loblolly
3	38	95.0	136	3	AAy44339 Arabidops
4	38	95.0	137	5	AAE25107 Arabidops
5	38	95.0	216	2	AAW98180 Arabidops
6	38	95.0	222	5	AAE25111 Arabidops
7	38	95.0	222	8	ADN72351 Thale cre
8	37	92.5	8	5	ABG65721 Plant ICK
9	37	92.5	8	5	ABG65712 Plant ICK
10	37	92.5	22	5	ABG65671 OsICK 1 p
11	37	92.5	38	3	AAE26247 Soybean C
12	37	92.5	38	3	AAPO1942 Soybean C
13	37	92.5	87	3	AAPO1951 Cyclin de
14	37	92.5	87	3	AAE27253 Soybean c
15	37	92.5	138	2	AAy08846 Murine mu
16	37	92.5	138	2	AAy08818 Murine p27
17	37	92.5	171	3	AAg42859 Arabidops
18	37	92.5	171	3	AAg15427 Arabidops
19	37	92.5	183	2	AAy08845 Murine mu
20	37	92.5	183	2	AAy08840 Murine mu
21	37	92.5	183	2	AAy08812 Murine p27
22	37	92.5	183	2	AAy08817 Murine p27
23	37	92.5	191	3	AAy44335 Arabidops
24	37	92.5	191	3	AAg15426 Arabidops
25	37	92.5	191	3	AAg42858 Arabidops

ALIGNMENTS

RESULT 1

ABG65714

ID ABG65714 standard; peptide; 8 AA.

XX ABG65714;

AC ABG65714;

XX 27-AUG-2002 (first entry)

XX Plant ICK protein conserved motif 1 #22.

XX Plant; inhibitor of cyclin dependent kinase; ICK.

XX Arabidopsis thaliana.

XX WO200228893-A2.

XX 11-APR-2002.

XX 29-JUN-2001; 2001WO-IB001492.

XX 14-JUL-2000; 2000US-0218471P.

XX 13-OCT-2000; 2000US-0241219P.

XX (CROP-) CROPDESIGN NV.

XX Frankard VMG, Peres Bota AM, Droual A, Mironov V, Inze D;

XX Hatzfeld Y;

XX WPI; 2002-471311/50.

XX Novel plant ICK (inhibitors of Cyclin Dependent Kinases) polypeptide used to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production of ICK inhibitors.

XX Disclosure; Page 14; 141pp; English.

XX This invention relates to the DNA and protein sequences of novel isolated ICK (inhibitors of Cyclin Dependent Kinases) proteins. The sequences of ICK (inhibitors of Cyclin Dependent Kinases) proteins characterised by the invention may be used for treating disorders characterised by insufficient or excessive production of an ICK inhibitor. The protein of the invention may also be used to screen for naturally-occurring ICK substrates, drugs or compounds which modulate ICK activity, as well as to treat disorders characterised by insufficient or excessive production of ICK protein, forms which have decreased or aberrant activity compared to ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention

```

SQ      Sequence 8 AA;
Query Match          95.0%; Score 38; DB 5; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      2 LSGRYEW 8
      | | | | |
      | | | | |

RESULT 2
ABG65677
ID      ABG65677 standard; protein; 53 AA.
XX
AC      ABG65677;
XX
DT      27-AUG-2002 (first entry)
XX
DE      Loblolly ICK protein.
XX
KW      Plant; inhibitor of cyclin dependent kinase; ICK.
XX
OS      Pinus taeda.
XX
XX      WO200228893-A2.
XX
PD      11-APR-2002.
XX
PF      29-JUN-2001; 2001WO-IB001492.
XX
PR      14-JUL-2000; 2000US-0218471P.
PR      13-OCT-2000; 2000US-0241219P.
XX
PA      (CROP-) CROPDDESIGN NV.
XX
PI      Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
PI      Hatzfeld Y;
XX
DR      WPI; 2002-471311/50.
XX
Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
PT to screen substrates, drugs or compounds which modulate ICK activity and
PT treat disorders characterized by an insufficient or excessive production
PT of ICK inhibitors.
XX
PS      Claim 48; Example 5; 141pp; English.
XX
This invention relates to the DNA and protein sequences of novel isolated
CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
CC the invention may be used for treating disorders characterised by
CC insufficient or excessive production of an ICK inhibitor. The protein of
CC the invention may also be used to screen for naturally-occurring ICK
CC substrates, drugs or compounds which modulate ICK activity, as well as to
CC treat disorders characterised by insufficient or excessive production of
CC ICK protein, forms which have decreased or aberrant activity compared to
CC ICK wild type protein. The present sequence represents an inhibitor of
CC cyclin dependent kinase (ICK) protein of the invention
XX
SQ      Sequence 53 AA;
Query Match          95.0%; Score 38; DB 5; Length 53;
Best Local Similarity 85.7%; Pred. No. 4.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      42 LSGRYEW 48
      | | | | |
      | | | | |

RESULT 3
AA44339
ID      AA44339 standard; protein; 136 AA.
XX
Query Match          95.0%; Score 38; DB 3; Length 136;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      125 LSGRYEW 131
      | | | | |
      | | | | |

RESULT 4
AAE25107
ID      AAE25107 standard; protein; 137 AA.
XX
AC      AAE25107;
XX
DT      30-OCT-2002 (first entry)
XX
DE      Arabidopsis thaliana ICN7 partial protein.
XX
Plant development; cyclin-dependent kinase; CDK inhibitor; ICK1; ICK2;
KW ICN2; ICN6; ICN7; ICN8; ICDK; morphogenesis; maturation; enlargement;
KW plant breeding; growth.
XX
XX

```

OS Arabidopsis thaliana.  
 XX WO200250292-A2.  
 XX PD 27-JUN-2002.  
 XX PF 18-DEC-2001; 2001WO-CA001825.  
 XX PR 18-DEC-2000; 2000US-0255908P.  
 XX PA (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.  
 XX PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.  
 XX PI Wang H, Zhou Y, Fowke LC;  
 XX WPI; 2002-519888/55.  
 XX DR N-PSDB; AAD40767.  
 XX CC Modifying plant development, e.g. growth or maturation, which is  
 PT particularly useful in plant breeding, by introducing nucleic acids  
 PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins  
 PT that bind to CDK inhibitors.  
 XX PS Disclosure; Fig 10A; 89pp; English.  
 XX CC The invention relates to a method for the development of a plant. The  
 CC method involves introducing into a plant cell a nucleic acid encoding a  
 CC protein that binds or interacts with a cyclin-dependent kinase (CDK)  
 CC inhibitor polypeptide (such as ICK1, ICK2, ICN2, ICN6, ICN7, ICN8 and  
 CC ICKX), a cyclin polypeptide, a CDK, or a polypeptide that modulates the  
 CC degradation of a CDK inhibitor polypeptide. The method is useful for  
 CC modifying the growth and development of plants e.g. morphogenesis,  
 CC growth, multiplication, enlargement, differentiation or maturation of a  
 CC cell or plant. It is particularly useful in plant breeding. The present  
 CC sequence is A. thaliana ICN7 partial protein  
 XX SQ Sequence 137 AA;  
 Query Match 95.0%; Score 38; DB 5; Length 137;  
 Best Local Similarity 85.7%; Pred. No. 11;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LXGRYEW 8  
 Db 126 LSGRYEW 132  
 RESULT 5  
 AAW98180  
 ID AAW98180 standard; protein; 216 AA.  
 XX AC AAW98180;  
 XX DT 05-JUL-1999 (first entry)  
 XX DE Arabidopsis cyclin-dependent kinase inhibitor FL66.  
 KW Cyclin-dependent kinase inhibitor; CDK inhibitor; CKI; CDKI; FL66;  
 KW plant development; transgenic plant; cell cycle; growth regulator;  
 KW herbicide.  
 XX OS Arabidopsis thaliana.  
 XX FH Key Location/Qualifiers  
 FT Protein 11..216  
 FT /note= "this protein region is specifically claimed in  
 FT Claim 1(c)"  
 XX WO9914331-A2.  
 XX PN 25-MAR-1999.  
 XX PD 16-SEP-1998; 98WO-EP005695.  
 XX PF

XX 16-SEP-1997; 97EP-00202838.  
 PR 24-DEC-1997; 97EP-00204111.  
 XX (CROP-) CROPDESIGN NV.  
 XX PI Inze D, De Veylder L, De Almeida J, Landrieu I;  
 XX WPI; 1999-229535/19.  
 XX DR N-PSDB; AAX25016.  
 XX PT DNA encoding inhibitor of cyclin-dependent kinase.  
 XX PS Claim 1a; Page 76-77; 89pp; English.  
 XX CC The present sequence is FL66, a new cyclin-dependent kinase (CDK)  
 CC inhibitor of Arabidopsis thaliana encoded by a cDNA clone (see AAX25016)  
 CC obtained by two-hybrid screening using CDC2AAT protein as bait. Results  
 CC established that several CDK inhibitors (see also AAW98179 and AAW98181)  
 CC exist in plants and that these inhibitors are expressed at different time  
 CC points and may have different functions during the development of the  
 CC plant. CDK inhibitors, nucleic acids, antibodies, promoter sequences,  
 CC related recombinant DNA and vectors are all useful: for diagnosis (no  
 CC details); for modulating the cycle, division and/or growth of plant cells  
 CC ; for altering activity of CDK; for modulating growth inhibition in  
 CC plants caused by environmental stress; for inducing male or female  
 CC sterility; for altering cell division progression in plants, bacteria,  
 CC fungi, insect and animal cells; and to screen for agonists or antagonists  
 CC that are potentially useful as growth regulators or herbicides. Plants of  
 CC any sort can be treated, e.g. to alter their size or resistance to  
 CC disease  
 XX SQ Sequence 216 AA;  
 Query Match 95.0%; Score 38; DB 2; Length 216;  
 Best Local Similarity 85.7%; Pred. No. 18;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LXGRYEW 8  
 Db 205 LSGRYEW 211  
 RESULT 6  
 AAE25111  
 ID AAE25111 standard; protein; 222 AA.  
 XX AC AAE25111;  
 XX DT 30-OCT-2002 (first entry)  
 XX DE Arabidopsis thaliana ICN7 full-length protein.  
 KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICK1; ICK2;  
 KW ICN2; ICN6; ICN7; ICN8; ICN9; morphogenesis; maturation; enlargement;  
 KW plant breeding; growth.  
 XX OS Arabidopsis thaliana.  
 XX PN WO200250292-A2.  
 XX PD 27-JUN-2002.  
 XX PF 18-DEC-2001; 2001WO-CA001825.  
 XX PR 18-DEC-2000; 2000US-0255908P.  
 XX PA (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.  
 XX PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.  
 XX PI Wang H, Zhou Y, Fowke LC;  
 XX WPI; 2002-519888/55.  
 XX DR

DR N-PSDB; AAD40771.  
 XX  
 PT Modifying plant development, e.g. growth or maturation, which is  
 PT particularly useful in plant breeding, by introducing nucleic acids  
 PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins  
 PT that bind to CDK inhibitors.  
 XX  
 PS Disclosure; Fig 10B; 89pp; English.  
 XX  
 CC The invention relates to a method for the development of a plant. The  
 CC method involves introducing into a plant cell a nucleic acid encoding a  
 CC protein that binds or interacts with a cyclin-dependent kinase (CDK)  
 CC inhibitor polypeptide (such as ICK1, ICK2, ICK3, ICK4, ICK5, ICK6, ICK7, ICK8 and  
 CC ICK9), a cyclin polypeptide, a CDK, or a polypeptide that modulates the  
 CC degradation of a CDK inhibitor polypeptide. The method is useful for  
 CC modifying the growth and development of plants e.g. morphogenesis,  
 CC growth, multiplication, enlargement, differentiation or maturation of a  
 CC cell or plant. It is particularly useful in plant breeding. The present  
 CC sequence is A. thaliana ICK7 full-length protein  
 XX  
 SQ Sequence 222 AA;  
 Query Match 95.0%; Score 38; DB 5; Length 222;  
 Best Local Similarity 85.7%; Pred. No. 18;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LKGRYEW 8  
 DB 211 LSGRYEW 217  
 RESULT 7  
 ADN72351  
 ID ADN72351 standard; protein; 222 AA.  
 AC  
 XX ADN72351;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 246.  
 XX  
 KW plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;  
 KW animal feed product; thale cress; cell wall biosynthesis;  
 KW nitrogen metabolism; carbon metabolism.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 FN WO2004035798-A2.  
 XX  
 PD 29-APR-2004.  
 XX  
 PF 20-OCT-2003; 2003WO-EP011659.  
 XX  
 PR 18-OCT-2002; 2002EP-00079408.  
 XX  
 PA (CROP-) CROPDESIGN NV.  
 XX  
 PI Inze D, De Veylder L, Vlieghe K;  
 XX  
 DR WPI: 2004-348466/32.  
 DR N-PSDB; ADN72350.  
 XX  
 XX Altering plant characteristics, useful for producing plants for enzyme or  
 PT pharmaceutical production comprising modifying in a plant, expression of  
 PT one or more nucleic acids and/or modifying level or activity of one or  
 PT more proteins.  
 XX  
 PS Claim 1; SEQ ID NO 246; 134pp; English.  
 XX  
 CC This invention relates to a novel method for altering one or more plant  
 CC characteristics. Specifically, it refers to identifying genes that are up  
 CC - or down-regulated in transgenic plants overexpressing the heterodimeric  
 CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to

CC alter plant characteristics accordingly. The present invention describes  
 CC generating transgenic plants for the production of growth regulators,  
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where  
 CC the altered plant characteristics are selected from increased yield or  
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture  
 CC or physiology, altered endoreduplication, biochemistry, signal  
 CC transduction, storage lipid mobilisation and/or altered photosynthesis.  
 CC each relative to the corresponding wild type plants. Accordingly, these  
 CC sequences can also be useful as positive or negative selectable markers  
 CC during transformation of cells or tissues. The identified genes play a  
 CC role in a variety of biological processes such as DNA replication, cell  
 CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as  
 CC transcription factors. This polypeptide sequence is thale cress protein  
 CC expressed by a gene upregulated 1.3 fold or more in plants overexpressing  
 CC the E2Fa/Dpa transcription factor, given in an exemplification of the  
 CC invention.  
 XX  
 SQ Sequence 222 AA;  
 Query Match 95.0%; Score 38; DB 8; Length 222;  
 Best Local Similarity 85.7%; Pred. No. 18;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LKGRYEW 8  
 DB 211 LSGRYEW 217  
 RESULT 8  
 ABG65721  
 ID ABG65721 standard; peptide; 8 AA.  
 AC  
 XX ABG65721;  
 XX  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE Plant ICK protein conserved motif 1 #29.  
 XX  
 KW Plant; inhibitor of cyclin dependent kinase; ICK.  
 XX  
 OS Oryza sativa.  
 XX  
 FN WO200228893-A2.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 29-JUN-2001; 2001WO-IB001492.  
 XX  
 PR 14-JUL-2000; 2000US-0218471P.  
 PR 13-OCT-2000; 2000US-0241219P.  
 XX  
 PA (CROP-) CROPDESIGN NV.  
 XX  
 PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;  
 PI Hatzfeld Y;  
 XX  
 DR WPI: 2002-471311/50.  
 XX  
 XX Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used  
 PT to screen substrates, drugs or compounds which modulate ICK activity and  
 PT treat disorders characterized by an insufficient or excessive production  
 PT of ICK inhibitors.  
 XX  
 PS Disclosure; Page 14; 141pp; English.  
 XX  
 CC This invention relates to the DNA and protein sequences of novel isolated  
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of  
 CC the invention may be used for treating disorders characterised by  
 CC insufficient or excessive production of an ICK inhibitor. The protein of  
 CC the invention may also be used to screen for naturally-occurring ICK  
 CC substrates, drugs or compounds which modulate ICK activity, as well as to  
 CC treat disorders characterised by insufficient or excessive production of  
 CC ICK protein, forms which have decreased or aberrant activity compared to

CC ICK wild type protein. The present sequence represents an inhibitor of  
 CC cyclin dependent kinase (ICK) protein of the invention

SQ Sequence 8 AA;

Query Match 92.5%; Score 37; DB 5; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 1.7e+06;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKGRYEW 8  
 | | | | |  
 Db 2 LQGRYEW 8

RESULT 9

ID ABG65712 standard; peptide; 8 AA.

XX AC ABG65712;

DT 27-AUG-2002 (first entry)

DE Plant ICK protein conserved motif 1 #20.

XX KW Plant; inhibitor of cyclin dependent kinase; ICK.

XX OS Arabidopsis thaliana.

PN WO200228893-A2.

PD 11-APR-2002.

PF 29-JUN-2001; 2001WO-1B001492.

XX PR 14-JUL-2000; 2000US-0218471P.

PR 13-OCT-2000; 2000US-0241219P.

XX PA (CROP-) CROPDESIGN NV.

XX PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;  
 PI Hatzfeld Y;

DR WPI; 2002-471311/50.

XX Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used  
 PT to screen substrates, drugs or compounds which modulate ICK activity and  
 PT treat disorders characterized by an insufficient or excessive production  
 PT of ICK inhibitors.

XX PS Disclosure; Page 14; 141pp; English.

XX This invention relates to the DNA and protein sequences of novel isolated  
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of  
 CC the invention may be used for treating disorders characterised by  
 CC insufficient or excessive production of an ICK inhibitor. The protein of  
 CC the invention may also be used to screen for naturally-occurring ICK  
 CC substrates, drugs or compounds which modulate ICK activity, as well as to  
 CC treat disorders characterised by insufficient or excessive production of  
 CC ICK protein, forms which have decreased or aberrant activity compared to  
 CC ICK wild type protein. The present sequence represents an inhibitor of  
 CC cyclin dependent kinase (ICK) protein of the invention

SQ Sequence 8 AA;

Query Match 92.5%; Score 37; DB 5; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 1.7e+06;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKGRYEW 8  
 | | | | |  
 Db 2 LQGRYEW 8

RESULT 10

ABG65671  
 ID ABG65671 standard; protein; 22 AA.

XX AC ABG65671;

DT 27-AUG-2002 (first entry)

DE OsICK 1 protein.

XX KW Plant; inhibitor of cyclin dependent kinase; ICK.

XX OS Oryza sativa.

PN WO200228893-A2.

PD 11-APR-2002.

PF 29-JUN-2001; 2001WO-1B001492.

XX PR 14-JUL-2000; 2000US-0218471P.

PR 13-OCT-2000; 2000US-0241219P.

XX PA (CROP-) CROPDESIGN NV.

XX PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;  
 PI Hatzfeld Y;

DR WPI; 2002-471311/50.

DR N-PSDB; ABK93951.

XX Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used  
 PT to screen substrates, drugs or compounds which modulate ICK activity and  
 PT treat disorders characterized by an insufficient or excessive production  
 PT of ICK inhibitors.

XX PS Claim 48; Fig 4; 141pp; English.

XX This invention relates to the DNA and protein sequences of novel isolated  
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of  
 CC the invention may be used for treating disorders characterised by  
 CC insufficient or excessive production of an ICK inhibitor. The protein of  
 CC the invention may also be used to screen for naturally-occurring ICK  
 CC substrates, drugs or compounds which modulate ICK activity, as well as to  
 CC treat disorders characterised by insufficient or excessive production of  
 CC ICK protein, forms which have decreased or aberrant activity compared to  
 CC ICK wild type protein. The present sequence represents an inhibitor of  
 CC cyclin dependent kinase (ICK) protein of the invention

XX SQ Sequence 22 AA;

Query Match 92.5%; Score 37; DB 5; Length 22;  
 Best Local Similarity 85.7%; Pred. No. 2.6;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKGRYEW 8  
 | | | | |  
 Db 11 LQGRYEW 17

RESULT 11

AAAB26247  
 ID AAB26247 standard; protein; 38 AA.

XX AC AAB26247;

DT 17-JAN-2001 (first entry)

XX DE Soybean cyclin-dependent kinase inhibitor #1.

XX KW Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;  
 CDKI; cell growth; herbicide.

OS Glycine max.  
 XX WO200060087-A2.  
 PN 12-OCT-2000.  
 PD 06-APR-2000; 2000WO-US009106.  
 XX 07-APR-1999; 99US-0128192P.  
 XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PA Klein TM, Weng Z, Cahoon RE;  
 PI WPI; 2000-679375/66.  
 XX N-PSDB; AAA95278.  
 DR Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.  
 XX Claim 10; Page 42; 58pp; English.  
 PS The present sequence is the soybean cyclin-dependent kinase inhibitor  
 XX (CDKI). Its coding sequence was isolated by searching a soybean seedling  
 CC cDNA library for sequences similar to those encoding the CDKI from  
 CC Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI  
 CC is involved in the cell cycle, and may promote or inhibit cell division  
 CC and growth. The protein and its coding sequence are useful in the  
 CC production of transgenic plants which produce increased or decreased  
 CC amounts of the CDKI protein, in the identification of herbicides, in  
 CC genetic and physical mapping and in the isolation of the CDKI gene in  
 CC other organisms  
 XX Sequence 38 AA;  
 SQ

Query Match 92.5%; Score 37; DB 3; Length 38;  
 Best Local Similarity 85.7%; Pred. No. 4.5;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8  
 | | | | |  
 Db 27 LGRYEW 33

RESULT 12  
 AAP01942  
 ID AAP01942 standard; protein; 38 AA.  
 AC AAP01942;  
 XX 01-NOV-2001 (first entry)  
 DT Soybean Cyclin dependent kinase inhibitor (CDKI) clone sl2.pk0008.d2.  
 XX Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean;  
 KW plant growth inhibitor.  
 XX Glycine max.  
 OS WO200060087-A2.  
 PN 12-OCT-2000.  
 PD 06-APR-2000; 2000WO-US009106.  
 XX 07-APR-1999; 99US-0128192P.  
 XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PA Klein TM, Weng Z, Cahoon RE;  
 PI WPI; 2000-679375/66.  
 XX N-PSDB; AAN02392.

XX Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.  
 XX Claim 10; Page 42; 58pp; English.  
 PS The invention describes a novel isolated polynucleotide comprising a  
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase  
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control  
 CC of cell division, growth and death. The nucleotide sequences can be used  
 CC in a vector to transform a host cell to produce the CDKI polypeptide.  
 CC They can also be used in methods for selecting and obtaining a nucleic  
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.  
 CC The encoded protein can be used in a method for evaluating a compound for  
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used  
 CC as herbicides. They can also be used to inhibit plant growth. The  
 CC polynucleotide sequences can be used in gene mapping and as genetic  
 CC markers. The sequence is the soybean CDKI clone sl2.pk0008.d2 as  
 CC described in the method of the invention  
 XX Sequence 38 AA;  
 SQ

Query Match 92.5%; Score 37; DB 3; Length 38;  
 Best Local Similarity 85.7%; Pred. No. 4.5;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8  
 | | | | |  
 Db 27 LGRYEW 33

RESULT 13  
 AAP01951  
 ID AAP01951 standard; protein; 87 AA.  
 XX AAP01951;  
 AC 01-NOV-2001 (first entry)  
 DT Cyclin dependent kinase inhibitor (CDKI) clone sl2.pk0008.d2:fls.  
 XX Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean;  
 KW plant growth inhibitor.  
 XX Glycine max.  
 OS WO200060087-A2.  
 PN 12-OCT-2000.  
 PD 06-APR-2000; 2000WO-US009106.  
 XX 07-APR-1999; 99US-0128192P.  
 XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PA Klein TM, Weng Z, Cahoon RE;  
 PI WPI; 2000-679375/66.  
 XX N-PSDB; AAN02401.  
 DR Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.  
 XX Claim 10; Fig 1; 58pp; English.  
 PS The invention describes a novel isolated polynucleotide comprising a  
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase  
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control  
 CC of cell division, growth and death. The nucleotide sequences can be used  
 CC in a vector to transform a host cell to produce the CDKI polypeptide.  
 CC They can also be used in methods for selecting and obtaining a nucleic  
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.



CC The encoded protein can be used in a method for evaluating a compound for  
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used  
 CC as herbicides. They can also be used to inhibit plant growth. The  
 CC polynucleotide sequences can be used in gene mapping and as genetic  
 CC markers. The sequence is the soybean CDKI clone s12.pk0008.d2.fis as  
 CC described in the method of the invention  
 XX  
 XX Sequence 87 AA;

Query Match 92.5%; Score 37; DB 3; Length 87;  
 Best Local Similarity 85.7%; Pred. No. 11;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 LKGRYEW 8  
 | | | | |  
 Db 76 LEGRYEW 82

RESULT 14  
 AAB27253  
 ID AAB27253 standard; protein; 87 AA.  
 XX  
 AC AAB27253;  
 XX  
 DT 17-JAN-2001 (first entry)  
 XX  
 DE Soybean cyclin-dependent kinase inhibitor #2.  
 XX  
 KW Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;  
 KW CDKI; cell growth; herbicide.  
 XX  
 OS Glycine max.  
 XX  
 XX WO200060087-A2.  
 PN  
 XX  
 PD 12-OCT-2000:  
 XX  
 PF 06-APR-2000; 2000WO-US009106.  
 XX  
 PR 07-APR-1999; 99US-0128192P.  
 XX  
 PA (DUPO ) DU FONT DE NEMOURS & CO E I.  
 XX  
 PI Klein TM, Weng Z, Cahoon RE;  
 XX  
 XX WPI; 2000-679375/66.  
 DR N-PSDB; AA95287.  
 XX  
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.  
 XX  
 PS Claim 10; Fig 1; 58pp; English.

CC The present sequence is the soybean cyclin-dependent kinase inhibitor  
 CC (CDKI). Its coding sequence was isolated by searching a soybean seedling  
 CC cDNA library for sequences similar to those encoding the CDKI from  
 CC Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI  
 CC is involved in the cell cycle, and may promote or inhibit cell division  
 CC and growth. The protein and its coding sequence are useful in the  
 CC production of transgenic plants which produce increased or decreased  
 CC amounts of the CDKI protein, in the identification of herbicides, in  
 CC genetic and physical mapping and in the isolation of the CDKI gene in  
 CC other organisms  
 XX  
 XX Sequence 87 AA;

Query Match 92.5%; Score 37; DB 3; Length 87;  
 Best Local Similarity 85.7%; Pred. No. 11;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 LKGRYEW 8  
 | | | | |  
 Db 76 LEGRYEW 82

## RESULT 15

AA08846  
 ID AA08846 standard; protein; 138 AA.  
 XX  
 AC AA08846;  
 XX  
 DT 13-AUG-1999 (first entry)  
 XX  
 DE Murine mutant p27 protein from clone #850.  
 XX  
 KW p163; murine; p27 inhibitor; p27-induced inhibition; cell proliferation;  
 KW p27 binding domain; Ran binding domain; detection; screening; malignancy;  
 KW tumour; mutant; p27 protein.  
 XX  
 OS Mus sp.  
 XX  
 PN EP926236-A1.  
 XX  
 PD 30-JUN-1999.  
 XX  
 PF 12-DEC-1998; 98EP-00123708.  
 XX  
 PR 20-DEC-1997; 97DE-01056975.  
 XX  
 PA (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.  
 XX  
 PI Eilers M, Buergin A, Sedlacek H;  
 XX  
 XX WPI; 1999-349237/30.  
 DR  
 XX  
 PT New p27-inhibiting protein p163 and DNA - useful for detection and/or  
 PT quantification of p163 mRNA.  
 XX  
 XX Disclosure; Page 28; 68pp; German.  
 XX  
 CC This invention describes (1) a protein that inhibits p27 and thereby  
 CC arrests p27-induced inhibition of cell proliferation, (2) the protein of  
 CC (1) comprising at least part of the amino acid sequence of murine p163.  
 CC (3) a protein that can be derived from the protein of (2) by deletion of  
 CC the p27 binding domain or the Ran binding domain, (4) a protein that can  
 CC be derived from the protein of (2) by deletion of all amino acid  
 CC sequences other than the p27 binding domain, (5) a protein that is the  
 CC human or other mammalian species homologue of a protein as in (1)-(4),  
 CC (6) DNA encoding the p163 protein, (7) antibodies and antibody fragments  
 CC that bind to the p27 binding domain of a protein as above, (8) antibodies  
 CC and antibody fragments that bind to the Ran binding domain of a protein  
 CC as above, (9) antisense nucleic acids complementary to portions of the  
 CC DNA of (6) between codons 121 and 467, (10) a nucleic acid construct  
 CC coding for an antisense nucleic acid as in (9) for inhibiting the  
 CC proliferation of a cell, in which DNA coding for the antisense nucleic  
 CC acid sequence is linked to at least one activation sequence and is  
 CC introduced into the target cell as naked DNA or as an insert in a  
 CC nonviral or viral vector and (11) a nucleic acid construct containing the  
 CC DNA of (6) linked to an activation sequence that permits expression of a  
 CC protein as above in a cell. The DNA of (6) can be used for detection  
 CC and/or quantification of p163 mRNA in cells and/or tissues, preferably by  
 CC Northern blotting, PCR or fluorescent in-situ hybridisation. The proteins  
 CC can be used to produce antibodies, which can be used to detect the  
 CC corresponding protein in cells, tissues or body fluids. The antisense  
 CC nucleic acids can be used to inhibit cell proliferation in vitro or in  
 CC vivo. The proteins can be used to screen for substances that inhibit the  
 CC interaction between the proteins and their cellular binding partners,  
 CC preferably using a two hybrid system or using an affinity system in which  
 CC p163 or its p27-binding domain is immobilised on a solid phase, the solid  
 CC phase is incubated with a test substance, and the inhibition of the  
 CC binding of a labelled binding partner of p163 (especially p27 or Ran) is  
 CC measured. Assays for p163 can be used to assess the malignancy of  
 CC tumours. This sequence represents a mutant mouse p27 protein sequence  
 CC isolated from clone #826 which is used to describe the method of the  
 CC invention

XX

SQ Sequence 138 AA;

Query Match 92.5%; Score 37; DB 2; Length 138;  
Best Local Similarity 85.7%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8  
| | | | |  
Db 55 LEGRYEW 61

Search completed: October 26, 2004, 15:36:52  
Job time : 45.6154 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 13.2308 Seconds  
(without alignments)  
40.099 Million cell updates/sec

Title: US-09-574-735C-35

Perfect score: 40

Sequence: 1 XLGRYEW 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	95.0	222	4	US-09-526-597D-4
2	37	92.5	135	3	US-09-215-221-56
3	37	92.5	180	3	US-09-215-221-50
4	37	92.5	180	3	US-09-215-221-55
5	37	92.5	193	3	US-09-215-221-53
6	37	92.5	194	3	US-09-215-221-51
7	37	92.5	194	3	US-09-215-221-52
8	37	92.5	195	3	US-09-215-221-54
9	37	92.5	197	1	US-08-275-983B-2
10	37	92.5	197	3	US-08-415-655-6
11	37	92.5	197	3	US-09-240-906-8
12	37	92.5	197	3	US-09-215-221-57
13	37	92.5	197	3	US-08-794-002-4
14	37	92.5	197	3	US-08-854-039B-4
15	37	92.5	197	4	US-09-483-597-8
16	37	92.5	197	4	US-08-765-702B-4
17	37	92.5	212	3	US-09-215-221-49
18	37	92.5	355	4	US-09-252-991A-22494
19	36	90.0	223	3	US-09-526-597D-6
20	34	85.0	70	4	US-08-902-572-20
21	34	85.0	80	4	US-09-457-568-18
22	34	85.0	80	4	US-09-457-646-18
23	34	85.0	80	4	US-09-516-065-18
24	34	85.0	167	4	US-08-902-572-18
25	34	85.0	177	4	US-09-457-568-12
26	34	85.0	177	4	US-09-457-646-12
27	34	85.0	177	4	US-09-516-065-12

#### ALIGNMENTS

##### RESULT 1

US-09-526-597D-4  
; Sequence 4, Application US/09526597D  
; Patent No. 6710227  
; GENERAL INFORMATION:  
; APPLICANT: De veylder, Lieven  
; APPLICANT: De Almeida, Janice  
; APPLICANT: Landrieu, Isabelle  
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof  
; FILE REFERENCE: 1187-2  
; CURRENT APPLICATION NUMBER: US/09/526,597D  
; CURRENT FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 222  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-526-597D-4

Query Match 95.0%; Score 38; DB 4; Length 222;  
Best Local Similarity 85.7%; Pred. No. 6.1;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8  
Db 211 LSGRYEW 217

##### RESULT 2

US-09-215-221-56  
; Sequence 56, Application US/09215221  
; Patent No. 6265562  
; GENERAL INFORMATION:  
; APPLICANT: EILERS, MARTIN  
; APPLICANT: BUERGIN, ANDREA  
; APPLICANT: SEDLACEK, HANS-HARALD  
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY  
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF  
; FILE REFERENCE: 025083/0132  
; CURRENT APPLICATION NUMBER: US/09/215,221  
; CURRENT FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 197 56 975.7  
; PRIOR FILING DATE: 1997-12-20  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 56  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Murine sp.

Sequence 6, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 1, Appli  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 6, Appli  
Sequence 22, Appli  
Sequence 22, Appli  
Sequence 26, Appli  
Sequence 26, Appli  
Sequence 26, Appli  
Sequence 2, Appli  
Sequence 6, Appli  
Sequence 2, Appli  
Sequence 2, Appli

34 85.0 178 3 US-08-794-002-6  
34 85.0 178 3 US-08-854-039B-6  
34 85.0 178 4 US-08-765-702B-6  
34 85.0 198 1 US-08-275-983B-1  
34 85.0 198 1 US-08-275-983B-3  
34 85.0 198 1 US-08-406-248-4  
34 85.0 198 3 US-08-897-333A-2  
34 85.0 198 3 US-09-240-906-6  
34 85.0 198 3 US-08-794-002-2  
34 85.0 198 3 US-08-794-002-22  
34 85.0 198 3 US-08-854-039B-2  
34 85.0 198 4 US-09-457-568-26  
34 85.0 198 4 US-09-457-646-26  
34 85.0 198 4 US-09-516-065-26  
34 85.0 198 4 US-09-483-597-6  
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34 85.0 198 4 US-09-378-517B-6  
34 85.0 209 4 US-09-526-597D-2

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; FEATURE:
; OTHER INFORMATION: mutated p27
US-09-215-221-56

Query Match          92.5%; Score 37; DB 3; Length 135;
Best Local Similarity 85.7%; Pred. No. 5.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      55 LEGRYEW 61

RESULT 3
US-09-215-221-50
; Sequence 50, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: EILERS, MARTIN
; APPLICANT: BUERGIN, ANDREA
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0192
; CURRENT APPLICATION NUMBER: US/09/215,221
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 197 56 975.7
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: mutated p27
US-09-215-221-50

Query Match          92.5%; Score 37; DB 3; Length 180;
Best Local Similarity 85.7%; Pred. No. 7.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      55 LEGRYEW 61

RESULT 4
US-09-215-221-55
; Sequence 55, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: EILERS, MARTIN
; APPLICANT: BUERGIN, ANDREA
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0192
; CURRENT APPLICATION NUMBER: US/09/215,221
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 197 56 975.7
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: mutated p27
US-09-215-221-55

Query Match          92.5%; Score 37; DB 3; Length 180;
Best Local Similarity 85.7%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      55 LEGRYEW 61

RESULT 5
US-09-215-221-53
; Sequence 53, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: EILERS, MARTIN
; APPLICANT: BUERGIN, ANDREA
; APPLICANT: SEDLACEK, HANS-HARALD
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0192
; CURRENT APPLICATION NUMBER: US/09/215,221
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 197 56 975.7
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: mutated p27
US-09-215-221-53

Query Match          92.5%; Score 37; DB 3; Length 193;
Best Local Similarity 85.7%; Pred. No. 8.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      65 LEGRYEW 71

RESULT 6
US-09-215-221-51
; Sequence 51, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: EILERS, MARTIN
; APPLICANT: BUERGIN, ANDREA
; APPLICANT: SEDLACEK, HANS-HARALD
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0192
; CURRENT APPLICATION NUMBER: US/09/215,221
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 197 56 975.7
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: mutated p27
US-09-215-221-51

Query Match          92.5%; Score 37; DB 3; Length 194;
Best Local Similarity 85.7%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      65 LEGRYEW 71
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Db 66 LEGRYEW 72

## RESULT 7

US-09-215-221-52  
; Sequence 52, Application US/09215221  
; Patent No. 6265562  
; GENERAL INFORMATION:  
; APPLICANT: EILERS, MARTIN  
; APPLICANT: BUERGIN, ANDREA  
; APPLICANT: SEDLACEK, HANS-HARALD  
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY  
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF  
; FILE REFERENCE: 026083/0192  
; CURRENT APPLICATION NUMBER: US/09/215,221  
; CURRENT FILING DATE: 1998-12-18  
; PRIOR FILING DATE: 1997-12-20  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 52  
; LENGTH: 194  
; TYPE: PRT  
; ORGANISM: Murine sp.  
; FEATURE:  
; OTHER INFORMATION: mutated p27  
US-09-215-221-52

Query Match 92.5%; Score 37; DB 3; Length 194;  
Best Local Similarity 85.7%; Pred. No. 8.4;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

Db 66 LEGRYEW 72

## RESULT 8

US-09-215-221-54  
; Sequence 54, Application US/09215221  
; Patent No. 6265562  
; GENERAL INFORMATION:  
; APPLICANT: EILERS, MARTIN  
; APPLICANT: BUERGIN, ANDREA  
; APPLICANT: SEDLACEK, HANS-HARALD  
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY  
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF  
; FILE REFERENCE: 026083/0192  
; CURRENT APPLICATION NUMBER: US/09/215,221  
; CURRENT FILING DATE: 1998-12-18  
; PRIOR FILING DATE: 1997-12-20  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 54  
; LENGTH: 195  
; TYPE: PRT  
; ORGANISM: Murine sp.  
; FEATURE:  
; OTHER INFORMATION: mutated p27  
US-09-215-221-54

Query Match 92.5%; Score 37; DB 3; Length 195;  
Best Local Similarity 85.7%; Pred. No. 8.4;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

Db 67 LEGRYEW 73

## RESULT 9

US-08-275-983B-2

; Sequence 2, Application US/08275983B  
; Patent No. 5688665  
; GENERAL INFORMATION:  
; APPLICANT: Massague, Joan  
; APPLICANT: Roberts, James M.  
; APPLICANT: Koff, Andrew  
; APPLICANT: Polyak, Kornelia  
; TITLE OF INVENTION: Isolated p27 Protein, Nucleic Acid Molecules  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/275,983B  
; FILING DATE: 13-SEP-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/179,045  
; FILING DATE: 07-JAN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: MII-079CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 197 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-275-983B-2

Query Match 92.5%; Score 37; DB 1; Length 197;  
Best Local Similarity 85.7%; Pred. No. 8.5;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

Db 70 LEGRYEW 76

## RESULT 10

US-08-415-655-6  
; Sequence 6, Application US/08415655  
; Patent No. 6025480  
; GENERAL INFORMATION:  
; APPLICANT: Massague, Joan  
; APPLICANT: Lee, Mong-hong  
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING  
; TITLE OF INVENTION: P75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF  
; TITLE OF INVENTION: SAME  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,655
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1747/47418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-415-655-6

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```

Query Match          92.5%; Score 37; DB 3; Length 197;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      2 LXGRYEW 8
      | | | | |
Db      70 LEGRYEW 76

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RESULT 11
US-09-240-906-8
; Sequence 8, Application US/09240906
; Patent No. 6245965
; GENERAL INFORMATION:
; APPLICANT: ROUSSEL, MARTINE F.
; APPLICANT: SWEYNE, RICHARD
; APPLICANT: ZINDY, FREDERIQUE
; APPLICANT: CUNNINGHAM, JUSTINE
; TITLE OF INVENTION: CELLS THAT LACK P19INK4D AND P27KIP1 ACTIVITY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 1340-1-025
; CURRENT APPLICATION NUMBER: US/09/240,906
; CURRENT FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-240-906-8

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```

Query Match          92.5%; Score 37; DB 3; Length 197;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      2 LXGRYEW 8
      | | | | |
Db      70 LEGRYEW 76

```

```

RESULT 12
US-09-215-221-57
; Sequence 57, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: EILERS, MARTIN
; APPLICANT: BUERGIN, ANDREA
; APPLICANT: SEDLACEK, HANS-HARALD

```

```

; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; FILE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0192
; CURRENT APPLICATION NUMBER: US/09/215,221
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 197 56 975.7
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Murine sp.
; US-09-215-221-57

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Query Match          92.5%; Score 37; DB 3; Length 197;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY      2 LXGRYEW 8
      | | | | |
Db      70 LEGRYEW 76

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RESULT 13
US-08-794-002-4
; Sequence 4, Application US/08794002
; Patent No. 6316208
; GENERAL INFORMATION:
; APPLICANT: Roberts, James M.
; APPLICANT: Porter, Peggy L.
; TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHODS FOR ITS
; TITLE OF INVENTION: PRODUCTION AND USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,002
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-794-002-4

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Query Match          92.5%; Score 37; DB 3; Length 197;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      2 LXGRYEW 8
      | | | | |
Db      70 LEGRYEW 76

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RESULT 14  
US-08-854-039B-4  
; Sequence 4, Application US/08854039B  
; Patent No. 6355774  
; GENERAL INFORMATION:  
; APPLICANT: Massague, Joan  
; APPLICANT: Roberts, James M.  
; APPLICANT: Koff, Andrew  
; APPLICANT: Polyak, Kornelia  
; TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHOD FOR ITS  
; TITLE OF INVENTION: PRODUCTION AND USE  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/854,039B  
; FILING DATE: 09-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: MIV-079.04  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 197 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-854-039B-4

Query Match 92.5%; Score 37; DB 3; Length 197;  
Best Local Similarity 85.7%; Pred. No. 8.5;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8  
| | | | |  
Db 70 LEGRYEW 76

RESULT 15  
US-09-483-597-8  
; Sequence 8, Application US/09483597  
; Patent No. 6589505  
; GENERAL INFORMATION:  
; APPLICANT: ROUSSEL, MARTINE F.  
; APPLICANT: SWEYNE, RICHARD  
; APPLICANT: ZINDY, FREDERIQUE  
; APPLICANT: CUNNINGHAM, JUSTINE  
; APPLICANT: SEGIL, NEIL  
; APPLICANT: CHEN, PING  
; TITLE OF INVENTION: CELLS THAT LACK P19INK4D AND P27KIP1 ACTIVITY AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 1340-1-025N  
; CURRENT APPLICATION NUMBER: US/09/483,597  
; CURRENT FILING DATE: 2000-01-14  
; EARLIER APPLICATION NUMBER: 60/117,719  
; EARLIER FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8

; LENGTH: 197  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-483-597-8  
Query Match 92.5%; Score 37; DB 4; Length 197;  
Best Local Similarity 85.7%; Pred. No. 8.5;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 LXGRYEW 8  
| | | | |  
Db 70 LEGRYEW 76  
Search completed: October 26, 2004, 15:34:19  
Job time : 13.2308 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 115.077 Seconds  
(without alignments)  
22.507 Million cell updates/sec

Title: US-09-574-735c-35

Perfect score: 40

Sequence: 1 XLGRYEW 8

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
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- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	95.0	53	15	US-10-333-006-17
2	38	95.0	132	16	US-10-767-701-55128
3	38	95.0	137	9	US-09-733-507-4
4	38	95.0	137	15	US-10-451-139-13
5	38	95.0	222	15	US-10-688-291-4
6	38	95.0	222	15	US-10-451-139-21
7	38	95.0	224	15	US-10-424-599-210190
8	37	92.5	22	15	US-10-333-006-11
9	37	92.5	48	15	US-10-424-599-153517
10	37	92.5	191	9	US-09-733-507-2
11	37	92.5	191	9	US-09-733-507-10
12	37	92.5	191	15	US-10-451-139-2
13	37	92.5	197	9	US-09-865-018-4

14	37	92.5	205	15	US-10-424-599-182928	Sequence 182928,
15	37	92.5	224	16	US-10-437-963-198574	Sequence 198574,
16	37	92.5	235	15	US-10-282-122A-43638	Sequence 43638, A
17	37	92.5	245	13	US-10-087-192-1161	Sequence 1161, Ap
18	36	90.0	95	16	US-10-767-701-36263	Sequence 36263, A
19	36	90.0	205	15	US-10-424-599-235800	Sequence 235800,
20	36	90.0	218	16	US-10-437-963-128205	Sequence 128205,
21	36	90.0	223	15	US-10-688-291-6	Sequence 6, Appli
22	36	90.0	231	15	US-10-282-122A-77900	Sequence 77900, A
23	36	90.0	248	15	US-10-425-114-59718	Sequence 59718, A
24	36	90.0	255	15	US-10-425-114-61054	Sequence 61054, A
25	35	87.5	85	16	US-10-767-701-37255	Sequence 37255, A
26	35	87.5	571	14	US-10-156-761-12275	Sequence 12275, A
27	34	85.0	70	8	US-08-902-572-20	Sequence 20, Appl
28	34	85.0	167	8	US-08-902-572-18	Sequence 18, Appl
29	34	85.0	176	9	US-09-733-507-11	Sequence 11, Appl
30	34	85.0	176	15	US-10-424-599-212181	Sequence 212181,
31	34	85.0	176	15	US-10-451-139-10	Sequence 10, Appl
32	34	85.0	178	9	US-09-865-018-6	Sequence 6, Appli
33	34	85.0	195	15	US-10-451-139-23	Sequence 23, Appl
34	34	85.0	196	9	US-09-733-507-16	Sequence 16, Appl
35	34	85.0	196	15	US-10-451-139-15	Sequence 15, Appl
36	34	85.0	198	9	US-09-865-018-2	Sequence 2, Appli
37	34	85.0	198	10	US-09-970-561-2	Sequence 2, Appli
38	34	85.0	198	13	US-10-087-192-1164	Sequence 1164, Ap
39	34	85.0	198	14	US-10-170-385-303	Sequence 303, App
40	34	85.0	198	14	US-10-458-108-9	Sequence 9, Appli
41	34	85.0	198	15	US-10-302-812-78	Sequence 78, Appl
42	34	85.0	207	15	US-10-451-139-12	Sequence 12, Appl
43	34	85.0	208	9	US-09-733-507-13	Sequence 13, Appl
44	34	85.0	209	15	US-10-688-291-2	Sequence 2, Appli
45	34	85.0	209	15	US-10-451-139-19	Sequence 19, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-333-006-17  
; Sequence 17, Application US/10333006  
; Publication No. US20040019926A1  
; GENERAL INFORMATION:  
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A111e S.  
; APPLICANT: Peres Bota, Adrian Marius  
; APPLICANT: Droual, Anne-Marie  
; APPLICANT: Mironov, Vladimir  
; APPLICANT: Inz, Dirk  
; APPLICANT: Hatfield, Yves  
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS  
; FILE REFERENCE: 1187-13  
; CURRENT APPLICATION NUMBER: US/10/333,006  
; PRIOR FILING DATE: 2003-01-14  
; PRIOR APPLICATION NUMBER: PCT/IB01/01492  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/218,471  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/241,219  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 53  
; TYPE: PRT  
; ORGANISM: Pinus taeda  
US-10-333-006-17

Query Match 95.0%; Score 38; DB 15; Length 53;  
Best Local Similarity 85.7%; Pred. No. 7.6;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 LXGRYEW 8  
| | | | |  
Db 42 LXGRYEW 48

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RESULT 2
US-10-767-701-55128
; Sequence 55128, Application US/10767701
; Publication No. US2004017284A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 55128
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 15724648.pep
US-10-767-701-55128

Query Match          95.0%; Score 38; DB 16; Length 132;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 LKGRYEW 8
Db  50 LSGRYEW 56

RESULT 3
US-09-733-507-14
; Sequence 14, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-733-507-14

Query Match          95.0%; Score 38; DB 9; Length 137;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 LKGRYEW 8
Db  126 LSGRYEW 132

RESULT 4
US-10-451-139-13
; Sequence 13, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
```

```
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-451-139-13

Query Match          95.0%; Score 38; DB 15; Length 137;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 LKGRYEW 8
Db  126 LSGRYEW 132

RESULT 5
US-10-688-291-4
; Sequence 4, Application US/10688291
; Publication No. US20040073969A1
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/10/688,291
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US/09/526,597D
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-688-291-4

Query Match          95.0%; Score 38; DB 15; Length 222;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 LKGRYEW 8
Db  211 LSGRYEW 217

RESULT 6
US-10-451-139-21
; Sequence 21, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
```

; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/255,908  
; PRIOR FILING DATE: 2000-12-18  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 222  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-451-139-21

Query Match 95.0%; Score 38; DB 15; Length 222;  
Best Local Similarity 85.7%; Pred. No. 27;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8  
| | | | |  
DB 211 LSGRYEW 217

RESULT 7  
US-10-424-599-210190  
; Sequence 210190, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 210190  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_3182C.1.1.pep  
US-10-424-599-210190

Query Match 95.0%; Score 38; DB 15; Length 224;  
Best Local Similarity 85.7%; Pred. No. 27;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8  
| | | | |  
DB 213 LSGRYEW 219

RESULT 8  
US-10-333-006-11  
; Sequence 11, Application US/10333006  
; Publication No. US20040019926A1  
; GENERAL INFORMATION:  
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A111e S.  
; APPLICANT: Peres Bota, Adrian Marius  
; APPLICANT: Droual, Anne-Marie  
; APPLICANT: Mironov, Vladimir  
; APPLICANT: Inz., Dirk  
; APPLICANT: Hatzfeld, Yves  
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS  
; FILE REFERENCE: 1187-13  
; CURRENT APPLICATION NUMBER: US/10/333,006  
; CURRENT FILING DATE: 2003-01-14  
; PRIOR APPLICATION NUMBER: PCT/IB01/01492  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/218,471  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/241,219  
; PRIOR FILING DATE: 2000-10-13

; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-333-006-11

Query Match 92.5%; Score 37; DB 15; Length 22;  
Best Local Similarity 85.7%; Pred. No. 5.4;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8  
| | | | |  
DB 11 LQGRYEW 17

RESULT 9  
US-10-424-599-153517  
; Sequence 153517, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 153517  
; LENGTH: 48  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_10964C.1.1.pep  
US-10-424-599-153517

Query Match 92.5%; Score 37; DB 15; Length 48;  
Best Local Similarity 85.7%; Pred. No. 11;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8  
| | | | |  
DB 37 LQGRYEW 43

RESULT 10  
US-09-733-507-2  
; Sequence 2, Application US/09733507  
; Patent No. US20010025379A1  
; GENERAL INFORMATION:  
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan  
; TITLE OF INVENTION: Cyclin Dependent Kinase Inhibitors as Plant Growth  
; FILE REFERENCE: 81601-3  
; CURRENT APPLICATION NUMBER: US/09/733,507  
; CURRENT FILING DATE: 2000-12-02  
; PRIOR APPLICATION NUMBER: CA 2,256,121  
; PRIOR FILING DATE: 1998-12-31  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-733-507-2

Query Match 92.5%; Score 37; DB 9; Length 191;  
Best Local Similarity 85.7%; Pred. No. 36;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      2 LXGRYEW 8
Db      181 LEGRYEW 187

RESULT 11
US-09-733-507-10
; Sequence 10, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; PRIOR FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-733-507-10

Query Match      92.5%; Score 37; DB 9; Length 191;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      181 LEGRYEW 187

RESULT 12
US-10-451-139-2
; Sequence 2, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-451-139-2

Query Match      92.5%; Score 37; DB 15; Length 191;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      181 LEGRYEW 187

RESULT 13
US-09-865-018-4
; Sequence 4, Application US/09865018
; Patent No. US2002011086A1
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Roberts, James M.
; APPLICANT: Koff, Andrew
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS
; PRODUCTION AND USE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,018
; FILING DATE: 24-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,039
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amlnc acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-865-018-4

Query Match      92.5%; Score 37; DB 9; Length 197;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      70 LEGRYEW 76

RESULT 14
US-10-424-599-182928
; Sequence 182928, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53233)B
; FILE REFERENCE: 38-21(53233)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182928
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Glycine max
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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136198C.1.pep
US-10-424-599-182928

Query Match      92.5%; Score 37; DB 15; Length 205;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
Db 194 LQRYEW 200

RESULT 15
US-10-437-963-198574
; Sequence 198574, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 198574
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_9421C.1.pep
US-10-437-963-198574

Query Match      92.5%; Score 37; DB 16; Length 225;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
Db 203 LQRYEW 209
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Search completed: October 26, 2004, 15:33:29  
Job time : 115.077 secs





A:Reference number: A54839; MUID:94306519; PMID:8033213

A:Accession: I49064

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-197 <RES>

A:Cross-references: UNIPROT:P46414; EMBL:U10440; NID:G532771; PIDN:AAA21149.1; PID:G5327

C:Keywords: cell cycle control

Query Match 92.5%; Score 37; DB 2; Length 197;

Best Local Similarity 85.7%; Pred. No. 3.8; 1; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

DB 70 LGRYEW 76

#### RESULT 3

C83587

hypothetical protein PA0462 [imported] - Pseudomonas aeruginosa (strain PAO1)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004

C:Accession: C83587

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen

A:Reference number: A82950; MUID:2043737; PMID:10984043

A:Accession: C83587

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-234 <STO>

A:Cross-references: UNIPROT:Q91656; GB:AE004484; GB:AE004091; NID:G9946320; PIDN:AA0385

A:Experimental source: strain PAO1

C:Genetics:

A:Gene: PA0462

Query Match 92.5%; Score 37; DB 2; Length 234;

Best Local Similarity 85.7%; Pred. No. 4.5;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

DB 87 LYGRYEW 93

#### RESULT 4

AI0271

L-ribulose-phosphate 4-epimerase (EC 5.1.3.4) [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004

C:Accession: AI0271

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;

Geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

Ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, N.

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AI0271

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-231 <KUR>

A:Cross-references: UNIPROT:Q82EE3; GB:AL590842; PIDN:CAC91037.1; PID:G15980231; GSPDB:G

C:Genetics:

A:Gene: araD

C:Superfamily: L-ribulose-phosphate 4-epimerase

C:Keywords: isomerase

Query Match 90.0%; Score 36; DB 2; Length 231;

Best Local Similarity 71.4%; Pred. No. 7;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

DB 137 IAGRYEW 143

#### RESULT 5

A75022

hypothetical protein PAB1224 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

C:Accession: A75022

R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure

A:Reference number: A75001

A:Accession: A75022

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-216 <KAW>

A:Cross-references: UNIPROT:Q9UXZ7; GB:AJ248288; GB:AL096836; NID:G5458960; PIDN:CAB5061

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: PAB1224

C:Superfamily: Alkaligenes eutrophus phosphoglycolate phosphatase

Query Match 87.5%; Score 35; DB 2; Length 216;

Best Local Similarity 71.4%; Pred. No. 10;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

DB 53 MGRYEW 59

#### RESULT 6

T36265

probable uroporphyrin-III C-methyltransferase / uroporphyrinogen-III synthase - Streptomyces

C:Species: Streptomyces coelicolor

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: T36265

R:Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1999

A:Reference number: Z21576

A:Accession: T36265

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-565 <MUR>

A:Cross-references: UNIPROT:Q9WX17; EMBL:AL079345; PIDN:CAB45351.1; GSPDB:GN00070; SCOED

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCODDB:SC68.15C

C:Superfamily: bifunctional uroporphyrin-III C-methyltransferase/uroporphyrinogen-III sy

Query Match 87.5%; Score 35; DB 2; Length 565;

Best Local Similarity 71.4%; Pred. No. 28;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

DB 334 VTGRYEW 340

#### RESULT 7

T36005

hypothetical protein SCC22.15c - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: T36005

R:Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, July 1999

A:Reference number: Z21574

A:Accession: T36005

A:Status: preliminary; translated from GB/EMBL/DBJ



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Best Local Similarity 71.4%; Pred.No. 15;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;

QY 2 LXGRYEW 8
   |   |   |
Db 185 LKGRYDW 191

RESULT 10
152718
gene p27Kip1 protein - human
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: I52718
R;Pietrapol, J.A.; Rohlander, S.K.; Sato, Y.; Papadopoulos, N.; Liu, B.; Friedman
Cancer Res. 55, 1206-1210, 1995
A;Title: Assignment of the human p27Kip1 gene to 12p13 and its analysis in leuk
A;Reference number: I52718; MUID:95198144; PMID:7892309
A;Accession: I52718
A;Status: preliminary; translated from GE/EMBL/DBD
A;Molecule type: DNA
A;Residues: 1-198 <RES>
A;Cross-references: UNIPROT:Q96TE0; GB:S76988; NID:g938402; PIDN:AAD14244.1; P
C;Genetics:
A;Gene: p27Kip1
A;Introns: 153/1

Query Match 85.0%; Score 34; DB 2; Length 198;
Best Local Similarity 71.4%; Pred.No. 15;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;

QY 2 LXGRYEW 8
   |   |   |
Db 70 LEGYEW 76

RESULT 11
T46140
hypothetical protein T3A5.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46140
R;Bloeker, H.; Yewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.; Quetier
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23024
A;Accession: T46140
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-209 <BLO>
A;Cross-references: UNIPROT:Q9SCR2; EMBL:AL132979
A;Experimental source: cultivar Columbia; BAC clone T3A5
C;Genetics:
A;Map position: 3
A;Introns: 109/3; 130/2; 185/2
A;Note: T3A5.10

Query Match 85.0%; Score 34; DB 2; Length 209;
Best Local Similarity 100.0%; Pred.No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GRYEW 8
   |   |   |
Db 200 GRYEW 204

RESULT 12
G83487
hypothetical protein PA1268 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G83487
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey
Adman, S.; Yuen, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Labig

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.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83487
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-314 <STO>
A;Cross-references: UNIPROT:P06971; GB:AE004556; GB:AE004091; NID:g9947194; PIDN:AAG0465
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA1268
C;Superfamily: proline racemase

Query Match      85.0%; Score 34; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GRYEW 8
DB      271 GRYEW 275

RESULT 13
S63401
hypothetical protein YNR069c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N3555
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: S63401
R;Duesterhoeft, A.; Ficeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62944
A;Accession: S63401
A;Molecule type: DNA
A;Residues: 1-489 <DUE>
A;Cross-references: UNIPROT:P53755; EMBL:Z71684; NID:G1302601; PID:e239850; PID:g1302602
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YNR069c
A;Cross-references: SGD:S0005352
A;Map position: 14R

Query Match      85.0%; Score 34; DB 2; Length 489;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
DB      467 LRGRYEW 473

RESULT 14
QSECFE
ferrichrome-iron receptor precursor - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 30-Jun-1988 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: F64738; S25196; S45219; S06358
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97428617; PMID:9278503
A;Accession: F64738
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-747 <BLAT>
A;Cross-references: UNIPROT:P06971; GB:AE000124; GB:U00096; NID:g1786339; PIDN:AAC73261.
A;Experimental source: strain K-12, substrain W61655
R;Coulton, J.W.; Mason, P.; Cameron, D.R.; Carmel, G.; Jean, R.; Rode, H.N.
J. Bacteriol. 165, 181-192, 1986
A;Title: Protein fusions of beta-galactosidase to the ferrichrome-iron receptor of Esche
A;Reference number: A25196; MUID:86085668; PMID:3079747

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A;Accession: A25196
A;Molecule type: DNA
A;Residues: 1-608; RP', 611-747 <COU>
A;Cross-references: GB:D26562; NID:g473770; PIDN:BAA05598.1; PID:g473809
A;Experimental source: strain K-12
R;Fujita, N.
submitted to the EMBL Data Library, January 1994
A;Reference number: S45181
A;Accession: S45219
A;Molecule type: DNA
A;Residues: 1-608; RP', 611-747 <FUJ>
A;Cross-references: EMBL:D26562; NID:g473770; PIDN:BAA05598.1; PID:g473809
A;Experimental source: strain K-12, substrain W3110
R;Burkhardt, R.; Braun, V.
Mol. Gen. Genet. 209, 49-55, 1987
A;Title: Nucleotide sequence of the fhvC and fhvD genes involved in iron (III) hydroxama
A;Reference number: A32650; MUID:88038363; PMID:2823072
A;Accession: S06358
A;Molecule type: DNA
A;Residues: 723-747 <BUR>
A;Cross-references: EMBL:X05810
C;Genetics:
A;Gene: fhvA; tonA
A;Map position: 4 min
C;Function:
A;Description: located in the outer membrane, binds the ferrichrome-iron ligand; interac
system
C;Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolog
C;Keywords: iron transport; membrane protein
F;1-33/Domain: signal sequence status predicted <SIG>
F;34-747/Product: ferrichrome-iron receptor #status predicted <MAT>
F;98-235/Domain: tonB-dependent receptor amino-terminal homology <TNN>
F;468-747/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>

Query Match      85.0%; Score 34; DB 1; Length 747;
Best Local Similarity 71.4%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
DB      482 LGGRYDW 488

RESULT 15
B85499
outer membrane receptor protein FhuA fhuA [imported] - Escherichia coli (strain O157:H7,
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85499
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85499
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-747 <STO>
A;Cross-references: UNIPROT:O8X901; GB:AE005174; NID:G12512871; PIDN:AAG54454.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: fhuA
C;Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolog

Query Match      85.0%; Score 34; DB 2; Length 747;
Best Local Similarity 71.4%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
DB      482 LGGRYDW 488

```

Wed Oct 27 09:35:40 2004

Search completed: October 26, 2004, 15:40:08  
Job time : 13.0769 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:27:03 ; Search time 44.6154 Seconds  
(without alignments)  
103.171 Million cell updates/sec

Title: US-09-574-735C-35  
Perfect score: 40  
Sequence: 1 XLXGRYEW 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	95.0	185	2 Q8GT28	Q8GT28 lycopersico
2	38	95.0	222	2 Q9FKB5	Q9FKB5 arabidopsis
3	37	92.5	163	2 Q93V92	Q93V92 nicotiana t
4	37	92.5	166	2 Q6T220	Q6T220 glycine max
5	37	92.5	166	2 AAS13377	AAS13377 glycine m
6	37	92.5	180	2 Q6T221	Q6T221 glycine max
7	37	92.5	180	2 AAS13376	AAS13376 glycine m
8	37	92.5	191	2 O04154	O04154 arabidopsis
9	37	92.5	191	2 O82809	O82809 arabidopsis
10	37	92.5	191	2 Q8LDX1	Q8LDX1 arabidopsis
11	37	92.5	192	2 Q9FS28	Q9FS28 pisum sativ
12	37	92.5	197	1 CDNB_MOUSE	P46414 mus musculu
13	37	92.5	197	2 O03769	O03769 rattus norv
14	37	92.5	197	2 Q35792	Q35792 rattus norv
15	37	92.5	197	2 Q8BG74	Q8BG74 m mus muscu
16	37	92.5	198	2 Q6T222	Q6T222 glycine max
17	37	92.5	198	2 Q6QWC3	Q6QWC3 anas platyr
18	37	92.5	198	2 Q8JIV2	Q8JIV2 gallus gall
19	37	92.5	198	2 AAS02099	AAS02099 anas plat
20	37	92.5	198	2 AAS13375	AAS13375 glycine m
21	37	92.5	205	2 Q6T223	Q6T223 glycine max
22	37	92.5	205	2 AAS13374	AAS13374 glycine m
23	37	92.5	234	2 Q91656	Q91656 pseudomonas
24	37	92.5	1063	2 Q8BTR3	Q8BTR3 synechococc
25	36	90.0	189	2 Q9LRY0	Q9LRY0 arabidopsis
26	36	90.0	210	2 Q8GT29	Q8GT29 lycopersico
27	36	90.0	231	2 Q8ZEE3	Q8ZEE3 versinia pe
28	36	90.0	267	2 Q8D0J2	Q8D0J2 versinia pe
29	36	90.0	267	2 AAS62245	AAS62245 versinia
30	36	90.0	403	2 Q9CN07	Q9CN07 pasteurilla
31	35	87.5	160	2 Q6PV56	Q6PV56 versinia ru

32 35 87.5 160 2 AAS89651  
33 35 87.5 216 2 Q9UXZ7-  
34 35 87.5 231 2 Q6D5T0  
35 35 87.5 565 2 Q9WX17  
36 35 87.5 571 2 Q8ZET5  
37 34 85.0 43 2 Q96AF4  
38 34 85.0 104 2 Q8XY31  
39 34 85.0 136 2 Q708J1  
40 34 85.0 136 2 CA82383  
41 34 85.0 144 2 Q9XAC3  
42 34 85.0 156 2 Q93YF6  
43 34 85.0 158 2 Q43806  
44 34 85.0 172 2 Q9BEA5  
45 34 85.0 178 1 CDNB\_MUSVI

## ALIGNMENTS

## RESULT 1

Q8GT28 PRELIMINARY; PRT; 185 AA.  
AC Q8GT28  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE P27KIP1-related-protein 2.  
GN Name=krp2;  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamnids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
[1]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Local;  
RA Babis B., Joubes J., Hernould M., Inze D., Raymond P., Chevalier C.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ441250; CAD29649.1; -.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0004961; F:cyclin-dependent protein kinase inhibitor a.; IEA.  
DR GO; GO:0007050; P:cell cycle arrest; IEA.  
DR InterPro; IPR003175; CDI.  
DR Pfam; PF02234; CDI; 1.  
SQ SEQUENCE 185 AA; 21189 MW; 48DCC89A5336C676 CRC64;

Query Match 95.0%; Score 38; DB 2; Length 185;  
Best Local Similarity 85.7%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8  
Db 174 LSGRYEW 180

## RESULT 2

Q9FKB5 PRELIMINARY; PRT; 222 AA.  
ID Q9FKB5  
AC Q9FKB5;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K24G6  
DE (Cyclin-dependent kinase inhibitor 3).  
GN Name=krp3;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID=3702;  
[1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=98403884; PubMed=9734815;

RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,  
 RA Tabata S.,  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.  
 RT Sequence features of the regions of 1,367,185 bp covered by 19  
 RT physically assigned P1 and PAC clones.",  
 RL DNA Res. 5:203-216(1998).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=21342510; PubMed=11449057;  
 RA de Veylder L., Beekman T., Beemster G.T.S., Kroes L., Terras F.,  
 RA Landrieu I., Van Der Schueren E., Maes S., Naudts M., Inze D.,  
 RT "Functional analysis of Cyclin-dependent kinase inhibitors of  
 RT Arabidopsis.",  
 RL Plant Cell 13:1653-1668(2001).  
 DR EMBL; AB012442; BAB09435.1; -.  
 DR EMBL; AJ301554; CAC41617.1; -.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.  
 DR GO; GO:0018301; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.  
 DR GO; GO:0007050; P:cell cycle arrest; IEA.  
 DR InterPro; IPR003175; CDI.  
 DR Pfam; PF02234; CDI; 1.  
 KW Cyclin; Kinase.  
 SQ SEQUENCE 222 AA; 24925 MW; 7A3EB2C9A29688A7 CRC64;  
 Query Match 95.0%; Score 38; DB 2; Length 222;  
 Best Local Similarity 85.7%; Pred. No. 14;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LXGRYEW 8  
 DB 211 LSGRYEW 217  
 RESULT 3  
 Q93V92 PRELIMINARY; PRT; 163 AA.  
 ID Q93V92  
 AC Q93V92  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE CDK/cyclin inhibitor.  
 GN Name=kisla; Synonyms=kisl1;  
 OS Nicotiana tomentosiformis (Tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamids; Solanales; Solanaceae; Nicotiana.  
 OC NCBI\_TaxID=4098;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=23369088; PubMed=12481070;  
 RA Jasinski S., Perennes C., Bergounieux C., Glab N.,  
 RT "Comparative Molecular and Functional Analyses of the Tobacco Cyclin-  
 RT dependent kinase inhibitor Nek1a and its spliced variant NtKIS1b.",  
 RL Plant Physiol. 130:1871-1882(2002).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP Grondard S.,  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ297906; CAC82733.1; -.  
 DR EMBL; AJ297904; CAC82731.1; -.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.  
 DR GO; GO:0007050; P:cell cycle arrest; IEA.  
 DR InterPro; IPR003175; CDI.  
 DR Pfam; PF02234; CDI; 1.  
 KW Cyclin.  
 SQ SEQUENCE 163 AA; 18301 MW; E154A59D491B66B7 CRC64;  
 Query Match 92.5%; Score 37; DB 2; Length 163;  
 Best Local Similarity 85.7%; Pred. No. 17;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LXGRYEW 8  
 DB 157 LSGRYEW 163  
 RESULT 4  
 Q6T220 PRELIMINARY; PRT; 166 AA.  
 ID Q6T220  
 AC Q6T220  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Cyclin-dependent kinase inhibitor 2;2 (Fragment).  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OC NCBI\_TaxID=3847;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP Li S., Reverdatto S., Nielsen N.C.,  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AV439104; AAS13377.1; -.  
 DR GO; GO:0016301; P:kinase activity; IEA.  
 DR InterPro; IPR003175; CDI.  
 DR Pfam; PF02234; CDI; 1.  
 KW Cyclin; Kinase.  
 FT NON TER 166  
 SQ SEQUENCE 166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;  
 Query Match 92.5%; Score 37; DB 2; Length 166;  
 Best Local Similarity 85.7%; Pred. No. 17;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LXGRYEW 8  
 DB 157 LSGRYEW 163  
 RESULT 5  
 AAS13377 PRELIMINARY; PRT; 166 AA.  
 ID AAS13377  
 AC AAS13377  
 DT 10-MAY-2004 (TrEMBLrel. 27, Created)  
 DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 10-MAY-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Cyclin-dependent kinase inhibitor 2;2 (Fragment).  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OC NCBI\_TaxID=3847;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP Li S., Reverdatto S., Nielsen N.C.,  
 RL "cDNA of cell-cycle genes in soybean cotyledons.",  
 RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AV439104; AAS13377.1; -.  
 DR Cyclin; Kinase.  
 KW NON TER 166  
 SQ SEQUENCE 166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;  
 Query Match 92.5%; Score 37; DB 2; Length 166;  
 Best Local Similarity 85.7%; Pred. No. 17;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LXGRYEW 8  
 DB 157 LSGRYEW 163  
 RESULT 6  
 Q6T221

ID Q6T2Z1 PRELIMINARY; PRT; 180 AA.  
 AC Q6T2Z1.  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Cyclin-dependent kinase inhibitor 2;1 (Fragment).  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RA Li S., Reverdatto S., Nielsen N.C.;  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY439103; AAS13376.1; -.  
 DR GO; GO:0016301; F:kinase activity; IEA.  
 DR InterPro; IPR003175; CDI.  
 DR Pfam; PF02234; CDI; 1.  
 KW Cyclin; Kinase.  
 FT NON\_TER 180 180  
 SQ SEQUENCE 180 AA; 20060 MW; 9E4ABBF0918246E7 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 180;  
 Best Local Similarity 85.7%; Pred. No. 19;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKGRYEW 8  
 | | | | |  
 DB 171 LEGRYEW 177

RESULT 7  
 AAS13376 PRELIMINARY; PRT; 180 AA.  
 ID AAS13376;  
 AC AAS13376;  
 DT 10-WAY-2004 (TrEMBLrel. 27, Created)  
 DT 10-WAY-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 10-WAY-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Cyclin-dependent kinase inhibitor 2;1 (Fragment).  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RA Li S., Reverdatto S., Nielsen N.C.;  
 RL "cDNA of cell-cycle genes in soybean cotyledons.";  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY439103; AAS13376.1; -.  
 KW Cyclin; Kinase.  
 FT NON\_TER 180 180  
 SQ SEQUENCE 180 AA; 20060 MW; 9E4ABBF0918246E7 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 180;  
 Best Local Similarity 85.7%; Pred. No. 19;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKGRYEW 8  
 | | | | |  
 DB 171 LEGRYEW 177

RESULT 8  
 O04154 PRELIMINARY; PRT; 191 AA.  
 ID O04154;  
 AC O04154;  
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cyclin-dependent kinase inhibitor protein.  
 OS Name=ICK1;

OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC euroids I; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RX MEDLINE=97242401; PubMed=9087400;  
 RA Wang H., Fowke L.C., Crosby W.L.;  
 RT "A plant cyclin-dependent kinase inhibitor gene.";  
 RL Nature 386:451-452(1997).  
 DR EMBL; U94772; AAC49698.1; -.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.  
 DR GO; GO:0016301; F:kinase activity; IEA.  
 DR GO; GO:0007050; P:cell cycle arrest; IEA.  
 DR InterPro; IPR003175; CDI.  
 DR Pfam; PF02234; CDI; 1.  
 KW Cyclin; Kinase.  
 SQ SEQUENCE 191 AA; 22239 MW; 0432BD4F626C07B5 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 191;  
 Best Local Similarity 85.7%; Pred. No. 20;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKGRYEW 8  
 | | | | |  
 DB 181 LEGRYEW 187

RESULT 9  
 O82809 PRELIMINARY; PRT; 191 AA.  
 ID O82809;  
 AC O82809;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Cyclin-dependent kinase inhibitor.  
 GN Name=ICK1; Synonyms=Atg23430;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC euroids I; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RX MEDLINE=98426383; PubMed=9753775;  
 RA Wang H., Qi Q., Schott P., Cutler A.J., Crosby W.L., Fowke L.C.;  
 RT "ICK1, a cyclin-dependent protein kinase inhibitor from Arabidopsis  
 thaliana interacts with both Cdc2a and CycD3, and its expression is  
 induced by abscisic acid.";  
 RL Plant J. 15:501-510(1998).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RA Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,  
 RA Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,  
 RA Somerville C.R., Venter J.C.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RN SEQUENCE FROM N.A.  
 RA Town C.D., Kaul S.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC003040; AAC23758.1; -.  
 DR EMBL; AF079587; AAC34660.1; -.  
 DR PIR; T01132; T01132.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.  
 DR GO; GO:0016301; F:kinase activity; IEA.  
 DR GO; GO:0007050; P:cell cycle arrest; IEA.  
 DR InterPro; IPR003175; CDI.  
 DR Pfam; PF02234; CDI; 1.

KW Cyclin; Kinase  
SQ SEQUENCE 191 AA; 22283 MW; 0477A91E277C46B2 CRC64;  
Query Match 92.5%; Score 37; DB 2; Length 191;  
Best Local Similarity 85.7%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 LXGRYEW 8  
Db 181 LEGRYEW 187  
RESULT 10  
Q8LDX1 PRELIMINARY; PRT; 191 AA.  
AC Q8LDX1  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Cyclin-dependent kinase inhibitor protein.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2208475; PubMed=12093376;  
RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,  
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
RT "Full-length messenger RNA sequences greatly improve genome  
RT annotation."  
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RA Feldmann K.,  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY085749; AAM62967.1; -.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.  
DR GO; GO:0016301; P:kinase activity; IEA.  
DR GO; GO:0007050; P:cell cycle arrest; IEA.  
DR InterPro; IPR003175; CDI.  
DR Pfam; PF02234; CDI; 1.  
KW Cyclin; Kinase.  
SQ SEQUENCE 191 AA; 22282 MW; 19B7A91E277C46B2 CRC64;  
Query Match 92.5%; Score 37; DB 2; Length 191;  
Best Local Similarity 85.7%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 LXGRYEW 8  
Db 181 LEGRYEW 187  
RESULT 11  
Q9FS28 PRELIMINARY; PRT; 192 AA.  
AC Q9FS28  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Cyclin dependent kinase inhibitor.  
GN Name=cki;  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]  
RP SEQUENCE FROM N.A.

RC TISSUE=Axillary bud;  
RA Shimizu-Sato S., Mori H.;  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB029483; BAB20860.1; -.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.  
DR GO; GO:0016301; P:kinase activity; IEA.  
DR GO; GO:0007050; P:cell cycle arrest; IEA.  
DR InterPro; IPR003175; CDI.  
DR Pfam; PF02234; CDI; 1.  
KW Cyclin; Kinase.  
SQ SEQUENCE 192 AA; 21921 MW; E76D73400085EB2 CRC64;  
Query Match 92.5%; Score 37; DB 2; Length 192;  
Best Local Similarity 85.7%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 LXGRYEW 8  
Db 181 LEGRYEW 187  
RESULT 12  
CDNE MOUSE  
ID CDNE MOUSE STANDARD; PRT; 197 AA.  
AC P46414;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase  
DE inhibitor p27) (p27Kip1).  
GN Name=Cdkn1b;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94306519; PubMed=8033213;  
RA Toyoshima H., Hunter T.;  
RT "p27, a novel inhibitor of G1 cyclin-Cdk protein kinase activity, is  
RT related to p21."  
RL Cell 78:67-74(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=94306518; PubMed=8033212;  
RA Polyak K., Lee M.-H., Eddington-Bromage H., Koff A., Roberts J.M.,  
RA Tempest P., Massague J.;  
RT "Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a  
RT potential mediator of extracellular antimetogenic signals."  
RL Cell 78:59-66(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Salivary gland;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Toshitoki S., Carninci P.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;



RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RP INTERACTION WITH NUP50, AND MUTAGENESIS.  
 RC STRAIN=BAUB/C;  
 RX MEDLINE=20271857; PubMed=10811608;  
 RA Mueller D., Thieke K., Buerger A., Dickmanns A., Eilers M.;  
 RT "Cyclin E-mediated elimination of p27 requires its interaction with  
 RL the nuclear pore-associated protein mNAP60.";  
 RL EMBO J. 19:2158-2180 (2000).  
 CC -!- FUNCTION: Involved in G1 arrest. May mediate TGF beta-induced G1  
 CC arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,  
 CC cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin  
 CC NUP50 is required for nuclear import and for degradation of  
 CC phosphorylated p27Kip1 after nuclear import.  
 CC -!- SUBUNIT: Interacts with NUP50.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- SIMILARITY: Belongs to the CDI family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; U10440; AAZ21149.1; -;  
 DR EMBL; U09968; AAA20335.1; -;  
 DR EMBL; BC014296; AAH14296.1; -;  
 DR EMBL; I49064; I49064.  
 DR HSP; P46527; IJUSU.  
 DR MGI; MGI:104565; Cdkn1b.  
 DR GO; GO:0004861; P:cyclin-dependent protein kinase inhibitor a. . . ; IDA.  
 DR GO; GO:0005515; P:protein binding; IPI.  
 DR GO; GO:0007050; P:cell cycle arrest; IDA.  
 DR GO; GO:0045736; P:negative regulation of CDK activity; IDA.  
 DR GO; GO:0008285; P:negative regulation of cell proliferation; IMP.  
 DR InterPro; IPR003175; CDI.  
 DR Pfam; PF02234; CDI; 1.  
 DR Cell cycle; Nuclear protein; Protein kinase inhibitor.  
 KW Cell cycle; Nuclear localization signal (Potential).  
 FT DOMAIN 153 169 Nuclear localization signal (Potential).  
 FT MUTAGEN 90 90 R->G: Loss of interaction with NUP50.  
 SQ SEQUENCE 197 AA; 22210 MW; 2D19A6CF8E6A650D CRC64;  
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 Best Local Similarity 85.7%; Pred. No. 21;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LXGRYEW 8  
 DB 70 LEGRYEW 76  
 RESULT 13  
 ID C08769 PRELIMINARY; PRT; 197 AA.  
 AC C08769;  
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE p27 kip1 (Cyclin kinase inhibitor) (Cyclin dependent kinase  
 DE inhibitor).  
 GN Name=p27Kip1;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kawada M., Yanagoe S., Murakami Y., Suzuki K., Mizuno S., Uehara Y.;  
 RT "Induction of p27Kip1 degradation and anchorage independence by Ras

RT through the MAP kinase signaling pathway.";  
 RL Oncogene 0:0-0(0).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Uehara Y.; (AUG-1996) to the EMBL/GenBank/DBJ databases.  
 RN Submitted (JUL-1997)  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RA Dastvan F., Reidy M.A.;  
 RT Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Iwanaga K., Komori H., Ohtani K.;  
 RT Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; D86924; BAA19960.1; -;  
 DR EMBL; AF015194; AAB71368.1; -;  
 DR EMBL; AV623024; AAT46041.1; -;  
 DR EMBL; AV623040; AAT46051.1; -;  
 DR HSP; P46527; IJUSU.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0004861; P:cyclin-dependent protein kinase inhibitor a. . . ; IEA.  
 DR GO; GO:0007050; P:cell cycle arrest; IEA.  
 DR InterPro; IPR003175; CDI.  
 DR Pfam; PF02234; CDI; 1.  
 DR Cyclin; Kinase.  
 KW Cyclin; Kinase.  
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 Query Match 92.5%; Score 37; DB 2; Length 197;  
 Best Local Similarity 85.7%; Pred. No. 21;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LXGRYEW 8  
 DB 70 LEGRYEW 76  
 RESULT 14  
 ID C035792 PRELIMINARY; PRT; 197 AA.  
 AC C035792;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE P27.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Spleen;  
 RX MEDLINE=97381761; PubMed=9218722;  
 RA Nomura H., Sawada Y., Fujinaga K., Ohtaki S.;  
 RT "Cloning and characterization of rat p27Kip1, a cyclin-dependent  
 RT kinase inhibitor.";  
 RL Gene 191:211-218 (1997).  
 DR EMBL; D83792; BAA21561.1; -;  
 DR HSP; P46527; IJUSU.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0004861; P:cyclin-dependent protein kinase inhibitor a. . . ; IEA.  
 DR GO; GO:0007050; P:cell cycle arrest; IEA.  
 DR InterPro; IPR003175; CDI.  
 DR Pfam; PF02234; CDI; 1.  
 SQ SEQUENCE 197 AA; 22112 MW; 55738078C2D555B2 CRC64;  
 Query Match 92.5%; Score 37; DB 2; Length 197;  
 Best Local Similarity 85.7%; Pred. No. 21;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LXGRYEW 8  
 DB 70 LEGRYEW 76

RESULT 15  
 Q8BG74 PRELIMINARY; PRT; 197 AA.  
 AC Q8BG74; (TREMBLrel. 23, Created)  
 DT 01-WAR-2003 (TREMBLrel. 23, Last annotation update)  
 DT 01-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length  
 DE enriched library, clone:B430307G09 product:cyclin-dependent kinase  
 DE inhibitor 1B (P27), full insert sequence (Mus musculus adult male  
 DE corpus striatum cDNA, RIKEN full-length enriched library.  
 DE clone:CG30007H22 product:cyclin-dependent kinase inhibitor 1B (P27),  
 DE full insert sequence) (Mus musculus adult male liver tumor cDNA, RIKEN  
 DE full-length enriched library, clone:C730029J05 product:cyclin-  
 DE dependent kinase inhibitor 1B (P27), full insert sequence).  
 GN Name=Cdkn1b;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
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 RN [100]

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK046676; BAC32833.1; -;  
 DR EMBL; AK047669; BAC33119.1; -;  
 DR EMBL; AK050240; BAC34141.1; -;  
 DR HSSP; P46527; 1JSU.  
 DR MGD; MGI:104565; Cdkn1b.  
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . . ; IDA.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0007050; P:cell cycle arrest; IDA.  
 DR GO; GO:0008285; P:negative regulation of cell proliferation; IMP.  
 DR GO; GO:0045736; P:negative regulation of cyclin dependent pro. . . ; IDA.  
 DR GO; GO:0008284; P:positive regulation of cell proliferation; IMP.  
 DR InterPro; IPR003175; CDI.  
 DR Pfam; PF02234; CDI; 1.  
 KW Cyclin; Kinase.  
 SQ SEQUENCE 197 AA; 22183 MW; BAC30D648B9BA3D6 CRC64;  
 Query Match 92.5%; Score 37; DB 2; Length 197;  
 Best Local Similarity 85.7%; Pred. No. 21;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 LXGRYEW 8  
 Db 70 LEGRYEW 76  
 Search completed: October 26, 2004, 15:39:27  
 Job time : 46.6154 secs

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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 55.7692 Seconds  
(without alignments)  
64.324 Million cell updates/sec

Title: US-09-574-735C-36

Perfect score: 32

Sequence: 1 EXEFFXXE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	81.2	10	5	ABG65743 Plant ICK
2	26	81.2	10	5	ABG65738 Plant ICK
3	26	81.2	10	5	ABG65737 Plant ICK
4	26	81.2	87	5	ABG65672 OsICK 3 p
5	26	81.2	108	5	ABG65676 Broom cor
6	26	81.2	262	5	ABG65670 OsICK 2 p
7	25	78.1	10	5	ABG65733 Plant ICK
8	25	78.1	10	5	ABG65739 Plant ICK
9	25	78.1	46	3	ABG65731 Plant ICK
10	25	78.1	46	3	ABG65731 Plant ICK
11	25	78.1	60	3	ABG65731 Plant ICK
12	25	78.1	60	3	ABG65731 Plant ICK
13	25	78.1	90	5	ABG65673 Soybean c
14	25	78.1	99	3	ABG65673 Soybean c
15	25	78.1	99	3	ABG65673 Soybean c
16	25	78.1	194	5	ABG65691 Rice cycl
17	25	78.1	205	3	ABG65691 Rice cycl
18	25	78.1	205	3	ABG65691 Rice cycl
19	25	78.1	312	5	ABG65691 Rice cycl
20	25	78.1	436	5	ABG65691 Rice cycl
21	24	75.0	10	5	ABG65736 Plant ICK
22	24	75.0	10	5	ABG65736 Plant ICK
23	24	75.0	53	5	ABG65677 Loblolly
24	24	75.0	87	3	ABG65677 Loblolly
25	24	75.0	87	3	ABG65677 Loblolly

26	24	75.0	88	3	ABG65743
27	24	75.0	136	3	ABG65743
28	24	75.0	137	5	ABG65743
29	24	75.0	176	2	ABG65743
30	24	75.0	196	3	ABG65743
31	24	75.0	196	3	ABG65743
32	24	75.0	196	5	ABG65743
33	24	75.0	216	2	ABG65743
34	24	75.0	222	5	ABG65743
35	24	75.0	222	8	ABG65743
36	24	75.0	246	7	ABG65743
37	24	75.0	338	4	ABG65743
38	24	75.0	340	3	ABG65743
39	24	75.0	455	4	ABG65743
40	24	75.0	545	4	ABG65743
41	24	75.0	574	2	ABG65743
42	24	75.0	583	5	ABG65743
43	24	75.0	660	6	ABG65743
44	24	75.0	738	4	ABG65743
45	24	75.0	753	2	ABG65743

#### ALIGNMENTS

RESULT 1  
ABG65743  
ID ABG65743 standard; peptide; 10 AA.  
XX AC ABG65743;  
XX AC  
XX 27-AUG-2002 (first entry)  
XX  
XX Plant ICK protein conserved motif 1 #51.  
XX  
XX Plant; inhibitor of cyclin dependent kinase; ICK.  
XX Sorghum bicolor.  
XX  
XX WO200228893-A2.  
XX  
XX 11-APR-2002.  
XX  
XX 29-JUN-2001; 2001WO-1B001492.  
XX  
XX 14-JUL-2000; 2000US-0218471P.  
XX  
XX 13-OCT-2000; 2000US-0241219P.  
XX  
XX (CROP-) CROPDESIGN NV.  
XX  
XX Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;  
XX Hatzfeld Y;  
XX  
XX WPI; 2002-471311/50.  
XX  
XX Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used  
XX to screen substrates, drugs or compounds which modulate ICK activity and  
XX treat disorders characterized by an insufficient or excessive production  
XX of ICK inhibitors.  
XX  
XX Disclosure; Page 14; 141pp; English.

XX This invention relates to the DNA and protein sequences of novel isolated  
XX ICK (inhibitors of Cyclin Dependent Kinases) proteins. The sequences of  
XX the invention may be used for treating disorders characterised by  
XX insufficient or excessive production of an ICK inhibitor. The protein of  
XX the invention may also be used to screen for naturally-occurring ICK  
XX substrates, drugs or compounds which modulate ICK activity, as well as to  
XX treat disorders characterised by insufficient or excessive production of  
XX ICK protein, forms which have decreased or aberrant activity compared to  
XX ICK wild type protein. The present sequence represents an inhibitor of  
XX cyclin dependent kinase (ICK) protein of the invention

```

SQ      Sequence 10 AA;
  Query Match      81.2%; Score 26; DB 5; Length 10;
  Best Local Similarity 50.0%; Pred. No. 7.7;
  Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 EXEXFFXXE 10
Db      1 EIEAFFAAAE 10

RESULT 2
ABG65738
ID      ABG65738 standard; peptide; 10 AA.
AC      ABG65738;
XX      AC
XX      27-AUG-2002 (first entry)
DE      Plant ICK protein conserved motif 1 #46.
XX      Plant; inhibitor of cyclin dependent kinase; ICK.
XX      Oryza sativa.
XX      WO200228893-A2.
XX      11-APR-2002.
XX      29-JUN-2001; 2001WO-IB001492.
XX      14-JUL-2000; 2000US-0218471P.
XX      13-OCT-2000; 2000US-0241219P.
XX      (CROP-) CROPDESIGN NV.
XX      Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
XX      Hatzfeld Y;
XX      Oryza sativa.
XX      WO200228893-A2.
XX      11-APR-2002.
XX      29-JUN-2001; 2001WO-IB001492.
XX      14-JUL-2000; 2000US-0218471P.
XX      13-OCT-2000; 2000US-0241219P.
XX      (CROP-) CROPDESIGN NV.
XX      Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
XX      Hatzfeld Y;
XX      WPI; 2002-471311/50.
XX      Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
XX      to screen substrates, drugs or compounds which modulate ICK activity and
XX      treat disorders characterized by an insufficient or excessive production
XX      of ICK inhibitors.
XX      Disclosure; Page 14; 141pp; English.
XX      This invention relates to the DNA and protein sequences of novel isolated
XX      ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
XX      the invention may be used for treating disorders characterised by
XX      insufficient or excessive production of an ICK inhibitor. The protein of
XX      the invention may also be used to screen for naturally-occurring ICK
XX      substrates, drugs or compounds which modulate ICK activity, as well as to
XX      treat disorders characterised by insufficient or excessive production of
XX      ICK protein, forms which have decreased or aberrant activity compared to
XX      ICK wild type protein. The present sequence represents an inhibitor of
XX      cyclin dependent kinase (ICK) protein of the invention
XX      Sequence 10 AA;
  Query Match      81.2%; Score 26; DB 5; Length 10;
  Best Local Similarity 50.0%; Pred. No. 7.7;
  Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 EXEXFFXXE 10
Db      1 EIEAFFAAAE 10

RESULT 3
ABG65737
ID      ABG65737 standard; peptide; 10 AA.
AC      ABG65737;
XX      AC
XX      27-AUG-2002 (first entry)
DE      Plant ICK protein conserved motif 1 #45.
XX      Plant; inhibitor of cyclin dependent kinase; ICK.
XX      Oryza sativa.
XX      WO200228893-A2.
XX      11-APR-2002.
XX      29-JUN-2001; 2001WO-IB001492.
XX      14-JUL-2000; 2000US-0218471P.
XX      13-OCT-2000; 2000US-0241219P.
XX      (CROP-) CROPDESIGN NV.
XX      Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
XX      Hatzfeld Y;
XX      WPI; 2002-471311/50.
XX      Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
XX      to screen substrates, drugs or compounds which modulate ICK activity and
XX      treat disorders characterized by an insufficient or excessive production
XX      of ICK inhibitors.
XX      Disclosure; Page 14; 141pp; English.
XX      This invention relates to the DNA and protein sequences of novel isolated
XX      ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
XX      the invention may be used for treating disorders characterised by
XX      insufficient or excessive production of an ICK inhibitor. The protein of
XX      the invention may also be used to screen for naturally-occurring ICK
XX      substrates, drugs or compounds which modulate ICK activity, as well as to
XX      treat disorders characterised by insufficient or excessive production of
XX      ICK protein, forms which have decreased or aberrant activity compared to
XX      ICK wild type protein. The present sequence represents an inhibitor of
XX      cyclin dependent kinase (ICK) protein of the invention
XX      Sequence 10 AA;
  Query Match      81.2%; Score 26; DB 5; Length 10;
  Best Local Similarity 50.0%; Pred. No. 7.7;
  Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 EXEXFFXXE 10
Db      1 EIEAFFAAAE 10

RESULT 4
ABG65672
ID      ABG65672 standard; protein; 87 AA.
AC      ABG65672;
XX      AC
XX      27-AUG-2002 (first entry)
DE      OsiCK 3 protein.
XX      OsiCK 3 protein.
XX      Plant; inhibitor of cyclin dependent kinase; ICK.
XX      Oryza sativa.
XX      WO200228893-A2.
XX      11-APR-2002.

```



CC substrates, drugs or compounds which modulate ICK activity, as well as to  
 CC treat disorders characterised by insufficient or excessive production of  
 CC ICK protein, forms which have decreased or aberrant activity compared to  
 CC ICK wild type protein. The present sequence represents an inhibitor of  
 CC cyclin dependent kinase (ICK) protein of the invention  
 XX  
 SQ Sequence 262 AA;

Query Match 81.2%; Score 26; DB 5; Length 262;  
 Best Local Similarity 50.0%; Pred. No. 2.1e-02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
 |||||  
 Db 217 EIEAFFAAE 226

RESULT 7  
 ABG65733  
 ID ABG65733 standard; peptide; 10 AA.  
 XX  
 AC ABG65733;  
 XX  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE Plant ICK protein conserved motif 1 #41.  
 XX  
 KW Plant; inhibitor of cyclin dependent kinase; ICK.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN WO200228893-A2.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 29-JUN-2001; 2001WO-IB001492.  
 XX  
 PR 14-JUL-2000; 2000US-0218471P.  
 XX  
 PR 13-OCT-2000; 2000US-0241219P.  
 XX  
 PA (CROP-) CROPDESIGN NV.  
 XX  
 PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;  
 PI Hatzfeld Y;  
 XX  
 DR WPI; 2002-471311/50.  
 XX  
 PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used  
 PT to screen substrates, drugs or compounds which modulate ICK activity and  
 PT treat disorders characterized by an insufficient or excessive production  
 PT of ICK inhibitors.  
 XX  
 PS Disclosure; Page 14; 141pp; English.  
 XX  
 CC This invention relates to the DNA and protein sequences of novel isolated  
 CC ICK (inhibitors of Cyclin Dependent Kinases) proteins. The sequences of  
 CC the invention may be used for treating disorders characterised by  
 CC insufficient or excessive production of an ICK inhibitor. The protein of  
 CC the invention may also be used to screen for naturally-occurring ICK  
 CC substrates, drugs or compounds which modulate ICK activity, as well as to  
 CC treat disorders characterised by insufficient or excessive production of  
 CC ICK protein, forms which have decreased or aberrant activity compared to  
 CC ICK wild type protein. The present sequence represents an inhibitor of  
 CC cyclin dependent kinase (ICK) protein of the invention  
 XX  
 SQ Sequence 10 AA;

Query Match 78.1%; Score 25; DB 5; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.3;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
 |||||  
 Db 1 EIEAFFAAE 10

RESULT 9  
 AAB26246  
 ID AAB26246 standard; protein; 46 AA.  
 XX  
 AC AAB26246;  
 XX  
 DT 17-JAN-2001 (first entry)  
 XX  
 DE Rice cyclin-dependent kinase inhibitor #1.  
 XX  
 KW Rice; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division;  
 XX

Query Match 78.1%; Score 25; DB 5; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.3;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
 |||||  
 Db 1 EIEAFFAAE 10

RESULT 9  
 AAB26246  
 ID AAB26246 standard; protein; 46 AA.  
 XX  
 AC AAB26246;  
 XX  
 DT 17-JAN-2001 (first entry)  
 XX  
 DE Rice cyclin-dependent kinase inhibitor #1.  
 XX  
 KW Rice; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division;  
 XX

Db 1 EIEDFFASAE 10  
 RESULT 8  
 ABG65739  
 ID ABG65739 standard; peptide; 10 AA.  
 XX  
 AC ABG65739;  
 XX  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE Plant ICK protein conserved motif 1 #47.  
 XX  
 KW Plant; inhibitor of cyclin dependent kinase; ICK.  
 XX  
 OS Oryza sativa.  
 XX  
 PN WO200228893-A2.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 29-JUN-2001; 2001WO-IB001492.  
 XX  
 PR 14-JUL-2000; 2000US-0218471P.  
 XX  
 PR 13-OCT-2000; 2000US-0241219P.  
 XX  
 PA (CROP-) CROPDESIGN NV.  
 XX  
 PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;  
 PI Hatzfeld Y;  
 XX  
 DR WPI; 2002-471311/50.  
 XX  
 PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used  
 PT to screen substrates, drugs or compounds which modulate ICK activity and  
 PT treat disorders characterized by an insufficient or excessive production  
 PT of ICK inhibitors.  
 XX  
 PS Disclosure; Page 14; 141pp; English.  
 XX  
 CC This invention relates to the DNA and protein sequences of novel isolated  
 CC ICK (inhibitors of Cyclin Dependent Kinases) proteins. The sequences of  
 CC the invention may be used for treating disorders characterised by  
 CC insufficient or excessive production of an ICK inhibitor. The protein of  
 CC the invention may also be used to screen for naturally-occurring ICK  
 CC substrates, drugs or compounds which modulate ICK activity, as well as to  
 CC treat disorders characterised by insufficient or excessive production of  
 CC ICK protein, forms which have decreased or aberrant activity compared to  
 CC ICK wild type protein. The present sequence represents an inhibitor of  
 CC cyclin dependent kinase (ICK) protein of the invention  
 XX  
 SQ Sequence 10 AA;

Query Match 78.1%; Score 25; DB 5; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.3;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
 |||||  
 Db 1 EIEAFFAAE 10

RESULT 9  
 AAB26246  
 ID AAB26246 standard; protein; 46 AA.  
 XX  
 AC AAB26246;  
 XX  
 DT 17-JAN-2001 (first entry)  
 XX  
 DE Rice cyclin-dependent kinase inhibitor #1.  
 XX  
 KW Rice; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division;  
 XX

Query Match 78.1%; Score 25; DB 5; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.3;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
 |||||  
 Db 1 EIEAFFAAE 10

RESULT 9  
 AAB26246  
 ID AAB26246 standard; protein; 46 AA.  
 XX  
 AC AAB26246;  
 XX  
 DT 17-JAN-2001 (first entry)  
 XX  
 DE Rice cyclin-dependent kinase inhibitor #1.  
 XX  
 KW Rice; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division;  
 XX

Query Match 78.1%; Score 25; DB 5; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.3;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
 |||||  
 Db 1 EIEAFFAAE 10

KW cell growth; herbicide.  
 XX  
 OS Oryza sativa.  
 XX  
 PN WC200060087-A2.  
 XX  
 XX  
 PD 12-OCT-2000.  
 XX  
 XX 06-APR-2000; 2000WO-US009106.  
 PF  
 XX 07-APR-1999; 99US-0128192P.  
 XX  
 PR (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PA  
 XX Klein TM, Weng Z, Cahoon RE;  
 PI  
 XX WPI; 2000-679375/66.  
 XX  
 DR N-PSDB; AAA95277.  
 DR  
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.  
 PT  
 XX  
 PS Claim 10; Page 40; 58pp; English.  
 XX  
 XX The present sequence is the rice cyclin-dependent kinase inhibitor  
 CC (CDKI). Its coding sequence was isolated by searching a rice leaf cDNA  
 CC library for sequences similar to those encoding the CDKI from *Chenopodium*  
 CC *rubrum*, *Caenorhabditis elegans* and *Arabidopsis thaliana*. CDKI is involved  
 CC in the cell cycle, and may promote or inhibit cell division and growth.  
 CC The protein and its coding sequence are useful in the production of  
 CC transgenic plants which produce increased or decreased amounts of the  
 CC CDKI protein, in the identification of herbicides, in genetic and  
 CC physical mapping and in the isolation of the CDKI gene in other organisms  
 XX  
 XX Sequence 46 AA;  
 SQ

Query Match 78.1%; Score 25; DB 3; Length 46;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 EXEXFFXXE 10  
 Db 6 ELEAFPAEE 15

RESULT 10  
 AAP01941  
 ID AAP01941 standard; protein; 46 AA.  
 XX  
 AC AAP01941;  
 XX  
 DT 01-NOV-2001 (first entry)  
 XX  
 DE Rice Cyclin dependent kinase inhibitor (CDKI) clone rsr9n.pk003.g12.  
 XX  
 KW Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; rice;  
 KW plant growth inhibitor.  
 XX  
 OS Oryza sativa.  
 XX  
 PN WC200060087-A2.  
 XX  
 PD 12-OCT-2000.  
 XX  
 XX 06-APR-2000; 2000WO-US009106.  
 PF  
 XX 07-APR-1999; 99US-0128192P.  
 XX  
 PR (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PA  
 XX Klein TM, Weng Z, Cahoon RE;  
 PI  
 XX WPI; 2000-679375/66.  
 XX  
 DR N-PSDB; AAA95277.  
 DR  
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.  
 PT  
 XX  
 PS Claim 10; Page 40; 58pp; English.  
 XX  
 XX The present sequence is the rice cyclin-dependent kinase inhibitor  
 CC (CDKI). Its coding sequence was isolated by searching a rice leaf cDNA  
 CC library for sequences similar to those encoding the CDKI from *Chenopodium*  
 CC *rubrum*, *Caenorhabditis elegans* and *Arabidopsis thaliana*. CDKI is involved  
 CC in the cell cycle, and may promote or inhibit cell division and growth.  
 CC The protein and its coding sequence are useful in the production of  
 CC transgenic plants which produce increased or decreased amounts of the  
 CC CDKI protein, in the identification of herbicides, in genetic and  
 CC physical mapping and in the isolation of the CDKI gene in other organisms  
 XX  
 XX Sequence 46 AA;  
 SQ

DR N-PSDB; AAN02391.  
 XX  
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.  
 XX  
 XX Claim 10; Page 40; 58pp; English.  
 XX  
 CC The invention describes a novel isolated polynucleotide comprising a  
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase  
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control  
 CC of cell division, growth and death. The nucleotide sequences can be used  
 CC in a vector to transform a host cell to produce the CDKI polypeptide.  
 CC They can also be used in methods for selecting and obtaining a nucleic  
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.  
 CC The encoded protein can be used in a method for evaluating a compound for  
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used  
 CC as herbicides. They can also be used to inhibit plant growth. The  
 CC polynucleotide sequences can be used in gene mapping and as genetic  
 CC markers. The sequence is the rice CDKI clone rsr9n.pk003.g12 as described  
 CC in the method of the invention  
 XX  
 SQ Sequence 46 AA;  
 SC

Query Match 78.1%; Score 25; DB 3; Length 46;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 EXEXFFXXE 10  
 Db 6 ELEAFPAEE 15

RESULT 11  
 AAP01953  
 ID AAP01953 standard; protein; 60 AA.  
 XX  
 AC AAP01953;  
 XX  
 DT 01-NOV-2001 (first entry)  
 XX  
 DE Cyclin dependent kinase inhibitor (CDKI) clone sl2.pk0117.h4.  
 XX  
 KW Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean;  
 KW plant growth inhibitor.  
 XX  
 OS Glycine max.  
 XX  
 PN WC200060087-A2.  
 XX  
 PD 12-OCT-2000.  
 XX  
 XX 06-APR-2000; 2000WO-US009106.  
 PF  
 XX 07-APR-1999; 99US-0128192P.  
 XX  
 PR (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PA  
 XX Klein TM, Weng Z, Cahoon RE;  
 PI  
 XX WPI; 2000-679375/66.  
 DR  
 DR N-PSDB; AAN02403.  
 XX  
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.  
 PT  
 XX  
 PS Claim 10; Fig 1; 58pp; English.  
 XX  
 XX The invention describes a novel isolated polynucleotide comprising a  
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase  
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control  
 CC of cell division, growth and death. The nucleotide sequences can be used  
 CC in a vector to transform a host cell to produce the CDKI polypeptide.  
 CC They can also be used in methods for selecting and obtaining a nucleic

CC acid sequence that encodes CDKI or affects the level of CDKI expression.  
 CC The encoded protein can be used in a method for evaluating a compound for  
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used  
 CC as herbicides. They can also be used to inhibit plant growth. The  
 CC polynucleotide sequences can be used in gene mapping and as genetic  
 CC markers. The sequence is the soybean CDKI clone s12.pk0117.h4 as  
 CC described in the method of the invention

XX Sequence 60 AA;

Query Match 78.1%; Score 25; DB 3; Length 60;  
 Best Local Similarity 50.0%; Pred. No. 82;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXEPFXXE 10  
 | | | | |  
 Db 19 ELEDFFAAAE 28

RESULT 12  
 AAB27255  
 ID AAB27255 standard; protein; 60 AA.

XX AAB27255;

DT 17-JAN-2001 (first entry)

DE Soybean cyclin-dependent kinase inhibitor #4.

KW Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;  
 KW CDKI; cell growth; herbicide.

OS Glycine max.

PN WO200060087-A2.

PD 12-OCT-2000.

XX 06-APR-2000; 2000WO-US009106.

XX 07-APR-1999; 99US-0128192P.

PA (DUPO ) DU PONT DE NEMOURS & CO E I.

PI Klein TM, Weng Z, Cahoon RE;

XX WPI; 2000-679375/66.

DR N-PSDB; AAA95289.

XX Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.

PS Claim 10; Fig 1; 58pp; English.

XX The present sequence is the soybean cyclin-dependent kinase inhibitor  
 CC (CDKI). Its coding sequence was isolated by searching a soybean seedling  
 CC cDNA library for sequences similar to those encoding the CDKI from  
 CC Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI  
 CC is involved in the cell cycle, and may promote or inhibit cell division  
 CC and growth. The protein and its coding sequence are useful in the  
 CC production of transgenic plants which produce increased or decreased  
 CC amounts of the CDKI protein, in the identification of herbicides, in  
 CC genetic and physical mapping and in the isolation of the CDKI gene in  
 CC other organisms

XX Sequence 60 AA;

Query Match 78.1%; Score 25; DB 3; Length 60;  
 Best Local Similarity 50.0%; Pred. No. 82;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXEPFXXE 10  
 | | | | |

Db 19 ELEDFFAAAE 28

RESULT 13

ABG5673

ID ABG5673 standard; protein; 90 AA.

XX ABG5673;

DT 27-AUG-2002 (first entry)

DE Rice Os ICK associated peptide.

KW Plant; inhibitor of cyclin dependent kinase; ICK.

XX Oryza sativa.

PN WO200228893-A2.

XX 11-APR-2002.

XX 29-JUN-2001; 2001WO-IB001492.

XX 14-JUL-2000; 2000US-0218471P.

PR 13-OCT-2000; 2000US-0241219P.

XX (CROP-) CROPDESIGN NV.

PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;

PI Hatzfeld Y;

XX WPI; 2002-471311/50.

XX Novel plant ICK (inhibitors of Cyclin Dependent Kinases) polypeptide used  
 PT to screen substrates, drugs or compounds which modulate ICK activity and  
 PT treat disorders characterized by an insufficient or excessive production  
 PT of ICK inhibitors.

XX Claim 48; Disclosure; 141pp; English.

XX This invention relates to the DNA and protein sequences of novel isolated  
 CC ICK (inhibitors of Cyclin Dependent Kinases) proteins. The sequences of  
 CC the invention may be used for treating disorders characterised by  
 CC insufficient or excessive production of an ICK inhibitor. The protein of  
 CC the invention may also be used to screen for naturally-occurring ICK  
 CC substrates, drugs or compounds which modulate ICK activity, as well as to  
 CC treat disorders characterised by insufficient or excessive production of  
 CC ICK protein, forms which have decreased or aberrant activity compared to  
 CC ICK wild type protein. The present sequence represents an inhibitor of  
 CC cyclin dependent kinase (ICK) protein of the invention

XX Sequence 90 AA;

Query Match 78.1%; Score 25; DB 5; Length 90;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXEPFXXE 10  
 | | | | |  
 Db 50 ELEAFPAEE 59

RESULT 14

AAB27251

ID AAB27251 standard; protein; 99 AA.

XX AAB27251;

DT 17-JAN-2001 (first entry)

DE Rice cyclin-dependent kinase inhibitor #2.

XX Rice; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division;



KW cell growth; herbicide.  
 XX Oryza sativa.  
 XX WO200060087-A2.  
 XX  
 PD 12-OCT-2000.  
 XX  
 PF 06-APR-2000; 2000WO-US009106.  
 XX  
 PR 07-APR-1999; 99US-0128192P.  
 XX  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Klein TM, Weng Z, Cahoon RE;  
 XX  
 DR WPI; 2000-679375/66.  
 XX N-PSDB; AAA95285.  
 XX  
 PT Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.  
 XX  
 PS Claim 10; Fig 1; 58pp; English.  
 XX  
 CC The present sequence is the rice cyclin-dependent kinase inhibitor  
 CC (CDKI). Its coding sequence was isolated by searching a rice leaf cDNA  
 CC library for sequences similar to those encoding the CDKI from *Chenopodium*  
 CC *rubrum*, *Caenorhabditis elegans* and *Arabidopsis thaliana*. CDKI is involved  
 CC in the cell cycle, and may promote or inhibit cell division and growth.  
 CC The protein and its coding sequence are useful in the production of  
 CC transgenic plants which produce increased or decreased amounts of the  
 CC CDKI protein, in the identification of herbicides, in genetic and  
 CC physical mapping and in the isolation of the CDKI gene in other organisms  
 XX  
 SQ Sequence 99 AA;  
 Query Match 78.1%; Score 25; DB 3; Length 99;  
 Best Local Similarity 50.0%; Pred. NO. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 EXEXFFXXXE 10  
 DB 59 ELEAFFAAEE 68  
 RESULT 15  
 AAP01949  
 ID AAP01949 standard; protein; 99 AA.  
 XX  
 AC AAP01949;  
 XX  
 DT 01-NOV-2001 (first entry)  
 XX  
 DE Cyclin dependent kinase inhibitor (CDKI) clone rsr9n.pk003.g12.fis.  
 XX  
 KW Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; rice;  
 KW plant growth inhibitor.  
 XX  
 OS Oryza sativa.  
 XX  
 FN WO200060087-A2.  
 XX  
 PD 12-OCT-2000.  
 XX  
 PF 06-APR-2000; 2000WO-US009106.  
 XX  
 PR 07-APR-1999; 99US-0128192P.  
 XX  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Klein TM, Weng Z, Cahoon RE;  
 XX  
 XX WPI; 2000-679375/66.

DR N-PSDB; AAN02399.  
 XX  
 PT Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.  
 XX  
 PS Claim 10; Fig 1; 58pp; English.  
 XX  
 CC The invention describes a novel isolated polynucleotide comprising a  
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase  
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control  
 CC of cell division, growth and death. The nucleotide sequences can be used  
 CC in a vector to transform a host cell to produce the CDKI polypeptide.  
 CC They can also be used in methods for selecting and obtaining a nucleic  
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.  
 CC The encoded protein can be used in a method for evaluating a compound for  
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used  
 CC as herbicides. They can also be used to inhibit plant growth. The  
 CC polynucleotide sequences can be used in gene mapping and as genetic  
 CC markers. The sequence is the rice CDKI clone rsr9n.pk003.g12.fis as  
 CC described in the method of the invention  
 XX  
 SQ Sequence 99 AA;  
 Query Match 78.1%; Score 25; DB 3; Length 99;  
 Best Local Similarity 50.0%; Pred. NO. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 EXEXFFXXXE 10  
 DB 59 ELEAFFAAEE 68  
 Search completed: October 26, 2004, 15:36:54  
 Job time : 57.7692 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 16.5385 Seconds  
(without alignments)  
40.099 Million cell updates/sec

Title: US-09-574-735C-36

Perfect score: 32

Sequence: 1 EXEFFFFXXE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pap.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pap.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pap.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	75.0	222	4	US-09-526-597D-4
2	24	75.0	583	3	US-09-311-311C-24
3	23	71.9	117	4	US-09-107-532A-6482
4	23	71.9	117	4	US-09-134-000C-5761
5	23	71.9	117	4	US-09-134-000C-6140
6	23	71.9	209	4	US-09-526-597D-2
7	23	71.9	860	4	US-09-248-796A-18585
8	23	71.9	966	4	US-09-688-188B-154
9	23	71.9	966	4	US-09-291-417D-154
10	23	71.9	968	4	US-09-688-188B-155
11	23	71.9	968	4	US-09-291-417D-107
12	23	71.9	968	4	US-09-291-417D-155
13	23	71.9	968	4	US-09-198-452A-1014
14	22	68.8	207	4	US-09-543-681A-7484
15	22	68.8	248	4	US-09-985-335-8
16	22	68.8	313	3	US-09-410-372-8
17	22	68.8	313	3	US-09-248-796A-25757
18	22	68.8	359	4	US-09-328-352-4855
19	22	68.8	408	4	US-09-985-335-3
20	22	68.8	440	3	US-09-410-372-3
21	22	68.8	440	3	US-08-860-519-12
22	22	68.8	600	3	US-09-489-039A-7380
23	22	68.8	600	3	US-09-297-937C-9
24	22	68.8	615	3	US-09-440-325A-1
25	22	68.8	694	3	US-09-846-996A-1
26	22	68.8	694	4	US-09-105-058C-23
27	22	68.8	722	4	US-09-105-058C-23

Sequence 89, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 34, Appli  
Sequence 20, Appli  
Sequence 2, Appli  
Sequence 96, Appli  
Sequence 74, Appli  
Sequence 34838, A  
Sequence 50055, A  
Sequence 4465, Ap  
Sequence 5436, Ap  
Sequence 4647, Ap  
Sequence 4940, Ap  
Sequence 5863, Ap  
Sequence 4385, Ap  
Sequence 61925, A

28 22 68.8 757 4 US-09-177-650-89  
29 22 68.8 844 4 US-09-813-148-4  
30 22 68.8 844 4 US-09-590-304-4  
31 22 68.8 844 4 US-09-492-361-34  
32 22 68.8 871 4 US-09-105-058C-20  
33 22 68.8 872 4 US-09-177-650-2  
34 22 68.8 930 4 US-09-177-650-96  
35 22 68.8 1276 3 US-09-297-937C-13  
36 21 65.6 29 4 US-09-079-030-74  
37 21 65.6 40 4 US-09-270-767-34838  
38 21 65.6 40 4 US-09-270-767-50055  
39 21 65.6 60 4 US-09-583-110-4465  
40 21 65.6 73 4 US-09-621-976-5436  
41 21 65.6 78 4 US-09-134-000C-4647  
42 21 65.6 94 3 US-09-134-001C-4940  
43 21 65.6 102 4 US-09-107-532A-5863  
44 21 65.6 104 4 US-09-107-532A-4385  
45 21 65.6 106 4 US-09-270-767-61925

ALIGNMENTS

RESULT 1  
US-09-526-597D-4  
; Sequence 4, Application US/09526597D  
; Patent No. 6710227  
; GENERAL INFORMATION:  
; APPLICANT: De Veylder, Lieven  
; APPLICANT: Landrieu, Isabelle  
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof  
; FILE REFERENCE: 1187-2  
; CURRENT APPLICATION NUMBER: US/09/526,597D  
; CURRENT FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 222  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-526-597D-4

Query Match 75.0%; Score 24; DB 4; Length 222;  
Best Local Similarity 50.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEFFFFXXE 10  
DB 181 EMEFFAYAE 190

RESULT 2  
US-09-311-311C-24  
; Sequence 24, Application US/093111311C  
; Patent No. 6358738  
; GENERAL INFORMATION:  
; APPLICANT: Erikson, et al.  
; TITLE OF INVENTION: POLO BOX THERAPEUTIC COMPOSITIONS,  
; TITLE OF INVENTION: METHODS, AND USES THEREFOR  
; FILE REFERENCE: 1874/117  
; CURRENT APPLICATION NUMBER: US/09/311,311C  
; CURRENT FILING DATE: 1999-05-13  
; PRIOR APPLICATION NUMBER: US 60/085,296  
; PRIOR FILING DATE: 1998-05-13  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 583  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURES:  
; NAME/KEY: CHAIN

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; LOCATION: (1)....(583)
; OTHER INFORMATION: GRASP65 protein
US-09-311-311C-24

Query Match          75.0%; Score 24; DB 3; Length 583;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 144 ESEDFTLIE 153

RESULT 3
US-09-107-532A-6482
; Sequence 6482, Application US/09107532A
; Patent No. 6563275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6482:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...117
; SEQUENCE DESCRIPTION: SEQ ID NO: 6482:
US-09-107-532A-6482

Query Match          71.9%; Score 23; DB 4; Length 117;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 65 EEESFFMWE 74

; LOCATION: (1)....(583)
; OTHER INFORMATION: GRASP65 protein
US-09-311-311C-24

Query Match          75.0%; Score 24; DB 3; Length 583;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 144 ESEDFTLIE 153

RESULT 3
US-09-107-532A-6482
; Sequence 6482, Application US/09107532A
; Patent No. 6563275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6482:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...117
; SEQUENCE DESCRIPTION: SEQ ID NO: 6482:
US-09-107-532A-6482

Query Match          71.9%; Score 23; DB 4; Length 117;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 65 EEESFFMWE 74
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RESULT 4
US-09-134-000C-5761
; Sequence 5761, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5761
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5761

Query Match          71.9%; Score 23; DB 4; Length 117;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 65 EEESFFMWE 74

RESULT 5
US-09-134-000C-6140
; Sequence 6140, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6140
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6140

Query Match          71.9%; Score 23; DB 4; Length 117;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 65 EEESFFMWE 74

RESULT 6
US-09-526-597D-2
; Sequence 2, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
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; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-526-597D-2

Query Match 71.9%; Score 23; DB 4; Length 209;  
Best Local Similarity 50.0%; Pred. No. 2.7e+02;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10  
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DB 164 ELEDFFQVAE 173

RESULT 7  
US-09-248-796A-18585  
; Sequence 18585, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 18585  
; LENGTH: 860  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-18585

Query Match 71.9%; Score 23; DB 4; Length 860;  
Best Local Similarity 50.0%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10  
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DB 298 ELETFFEXRE 307

RESULT 8  
US-09-688-188B-154  
; Sequence 154, Application US/09688188B  
; Patent No. 6656716  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0328  
; CURRENT APPLICATION NUMBER: US/09/688,188B  
; CURRENT FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 09/291,417  
; PRIOR FILING DATE: 1999-04-14  
; PRIOR APPLICATION NUMBER: 60/081,784  
; PRIOR FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 154  
; LENGTH: 966  
; TYPE: PRT  
; ORGANISM: Murine sp.  
US-09-688-188B-154

Query Match 71.9%; Score 23; DB 4; Length 966;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 EXEXFFXXXE 10  
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DB 933 EQEMFFKLSE 942

RESULT 9  
US-09-291-417D-154  
; Sequence 154, Application US/09291417D  
; Patent No. 6680170  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0329  
; CURRENT APPLICATION NUMBER: US/09/291,417D  
; CURRENT FILING DATE: 1999-04-13  
; PRIOR APPLICATION NUMBER: 60/081,784  
; PRIOR FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 154  
; LENGTH: 966  
; TYPE: PRT  
; ORGANISM: Murine sp.  
US-09-291-417D-154

Query Match 71.9%; Score 23; DB 4; Length 966;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10  
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DB 933 EQEMFFKLSE 942

RESULT 10  
US-09-688-188B-107  
; Sequence 107, Application US/09688188B  
; Patent No. 6656716  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0328  
; CURRENT APPLICATION NUMBER: US/09/688,188B  
; CURRENT FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 09/291,417  
; PRIOR FILING DATE: 1999-04-14  
; PRIOR APPLICATION NUMBER: 60/081,784  
; PRIOR FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 107  
; LENGTH: 968  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-688-188B-107

Query Match 71.9%; Score 23; DB 4; Length 968;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10  
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DB 934 EQEMFFKLSE 943

RESULT 11  
US-09-688-188B-155

; Sequence 155, Application US/09688188B  
; Patent No. 6656716  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0328  
; CURRENT APPLICATION NUMBER: US/09/688,188B  
; CURRENT FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 09/291,417  
; PRIOR FILING DATE: 1999-04-14  
; PRIOR APPLICATION NUMBER: 60/081,784  
; PRIOR FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 155  
; TYPE: PRT  
; LENGTH: 968  
; ORGANISM: Homo sapiens  
US-09-688-188B-155

Query Match 71.9%; Score 23; DB 4; Length 968;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
| | | | |  
Db 934 EQEMFFKLS 943

RESULT 12  
US-09-291-417D-107  
; Sequence 107, Application US/09291417D  
; Patent No. 6680170  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0329  
; CURRENT APPLICATION NUMBER: US/09/291,417D  
; CURRENT FILING DATE: 1999-04-13  
; PRIOR APPLICATION NUMBER: 60/081,784  
; PRIOR FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 107  
; LENGTH: 968  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-291-417D-107

Query Match 71.9%; Score 23; DB 4; Length 968;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
| | | | |  
Db 934 EQEMFFKLS 943

RESULT 13  
US-09-291-417D-155  
; Sequence 155, Application US/09291417D  
; Patent No. 6680170  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0329  
; CURRENT APPLICATION NUMBER: US/09/291,417D

; CURRENT FILING DATE: 1999-04-13  
; PRIOR APPLICATION NUMBER: 60/081,784  
; PRIOR FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 155  
; LENGTH: 968  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-291-417D-155

Query Match 71.9%; Score 23; DB 4; Length 968;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
| | | | |  
Db 934 EQEMFFKLS 943

RESULT 14  
US-09-198-452A-1014  
; Sequence 1014, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Griffais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 1014  
; LENGTH: 207  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-1014

Query Match 68.8%; Score 22; DB 4; Length 207;  
Best Local Similarity 66.7%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EXEXFF 6  
| | | | |  
Db 123 EAETFF 128

RESULT 15  
US-09-543-681A-7484  
; Sequence 7484, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY, BRETTON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 7484  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-7484

Query Match 68.8%; Score 22; DB 4; Length 248;  
Best Local Similarity 66.7%; Pred. No. 5.5e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EXEXFF 6

Wed Oct 27 09:35:40 2004

Db 128 ESEAFF 133

Search completed: October 26, 2004, 15:34:20  
Job time : 17.5385 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 143.846 Seconds  
(without alignments)  
22.507 Million cell updates/sec

Title: US-09-574-735C-36

Perfect score: 32

Sequence: 1 EXEFFFFXXE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
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11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
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20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	81.2	87	US-10-333-006-12	Sequence 12, Appl
2	26	81.2	108	US-10-333-006-16	Sequence 16, Appl
3	26	81.2	225	US-10-437-963-198574	Sequence 198574,
4	26	81.2	262	US-10-333-006-10	Sequence 10, Appl
5	26	81.2	417	US-10-437-963-195115	Sequence 195115,
6	25	78.1	90	US-10-333-006-13	Sequence 13, Appl
7	25	78.1	95	US-10-767-701-36263	Sequence 36263, A
8	25	78.1	194	US-10-333-006-44	Sequence 44, Appl
9	25	78.1	194	US-10-437-963-120870	Sequence 120870,
10	25	78.1	205	US-10-424-599-182928	Sequence 182928,
11	25	78.1	218	US-10-437-963-128205	Sequence 128205,
12	25	78.1	248	US-10-425-114-59718	Sequence 59718, A
13	25	78.1	255	US-10-425-114-61054	Sequence 61054, A

14	78.1	401	14	US-10-369-493-22727	Sequence 22727, A
15	78.1	401	14	US-10-369-493-22728	Sequence 22728, A
16	78.1	401	14	US-10-369-493-22808	Sequence 22808, A
17	75.0	53	15	US-10-333-006-17	Sequence 17, Appl
18	75.0	69	16	US-10-767-701-53471	Sequence 53471, A
19	75.0	137	9	US-09-733-507-14	Sequence 14, Appl
20	75.0	137	15	US-10-451-139-13	Sequence 13, Appl
21	75.0	176	15	US-10-424-599-212181	Sequence 212181,
22	75.0	196	9	US-09-733-507-15	Sequence 15, Appl
23	75.0	196	15	US-10-451-139-15	Sequence 15, Appl
24	75.0	205	15	US-10-424-599-235800	Sequence 235800,
25	75.0	222	15	US-10-688-291-4	Sequence 4, Appl
26	75.0	222	15	US-10-451-139-21	Sequence 21, Appl
27	75.0	246	14	US-10-104-047-2319	Sequence 2319, Ap
28	75.0	340	14	US-10-013-477-14	Sequence 14, Appl
29	75.0	570	16	US-10-437-963-177783	Sequence 177783,
30	75.0	617	16	US-10-437-963-177786	Sequence 177786,
31	75.0	660	15	US-10-282-122A-55169	Sequence 55169, A
32	75.0	786	14	US-10-369-493-6228	Sequence 6228, Ap
33	75.0	795	14	US-10-156-761-9635	Sequence 9635, Ap
34	75.0	905	13	US-10-114-893-127	Sequence 127, Ap
35	75.0	915	9	US-09-880-192-59	Sequence 59, Appl
36	75.0	915	14	US-10-427-348-59	Sequence 59, Appl
37	71.9	72	11	US-09-864-408A-8656	Sequence 8656, Ap
38	71.9	176	9	US-09-733-507-11	Sequence 11, Appl
39	71.9	176	15	US-10-451-139-10	Sequence 10, Appl
40	71.9	191	9	US-09-733-507-2	Sequence 2, Appl
41	71.9	191	9	US-09-733-507-10	Sequence 10, Appl
42	71.9	191	15	US-10-451-139-2	Sequence 2, Appl
43	71.9	209	15	US-10-688-291-2	Sequence 2, Appl
44	71.9	209	15	US-10-451-139-19	Sequence 19, Appl
45	71.9	276	14	US-10-156-761-9715	Sequence 9715, Ap

#### ALIGNMENTS

#### RESULT 1

US-10-333-006-12  
; Sequence 12, Application US/10333006  
; Publication No. US20040019926A1  
; GENERAL INFORMATION:  
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A1lle S.  
; APPLICANT: Peres Bota, Adrian Marius  
; APPLICANT: Drouot, Anne-Marie  
; APPLICANT: Mironov, Vladimir  
; APPLICANT: Inz, Dirk  
; APPLICANT: Hatzfeld, Yves  
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS  
; FILE REFERENCE: 1187-13  
; CURRENT APPLICATION NUMBER: US/10/333,006  
; CURRENT FILING DATE: 2003-01-14  
; PRIOR APPLICATION NUMBER: PCT/IB01/01492  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/218,471  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/241,219  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-333-006-12

Query Match 81.2%; Score 26; DB 15; Length 87;  
Best Local Similarity 50.0%; Pred. No. 99;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEFFFFXXE 10

DB 67 EIEAFFAAAE 76

RESULT 2  
 US-10-333-006-16  
 ; Sequence 16, Application US/10333006  
 ; Publication No. US20040019926A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Frankard, Valerie Marie-No. US20040019926A1lie S.  
 ; APPLICANT: Peres Bota, Adrian Marius  
 ; APPLICANT: Droual, Anne-Marie  
 ; APPLICANT: Mironov, Vladimir  
 ; APPLICANT: Inz., Dirk  
 ; APPLICANT: Hatzfeld, Yves  
 ; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS  
 ; FILE REFERENCE: 1187-13  
 ; CURRENT APPLICATION NUMBER: US/10/333,006  
 ; PRIOR FILING DATE: 2003-01-14  
 ; PRIOR APPLICATION NUMBER: PCT/IB01/01492  
 ; PRIOR FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/218,471  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: US 60/241,219  
 ; NUMBER OF SEQ ID NOS: 59  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 16  
 ; LENGTH: 108  
 ; TYPE: PRT  
 ; ORGANISM: Sorghum bicolor  
 US-10-333-006-16

Query Match 81.2%; Score 26; DB 15; Length 108;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEFPFXXE 10  
 DB 67 EIEAFFAAAE 76

RESULT 3  
 US-10-437-963-198574  
 ; Sequence 198574, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 198574  
 ; LENGTH: 225  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_9421C.1.pep  
 US-10-437-963-198574

Query Match 81.2%; Score 26; DB 16; Length 225;  
 Best Local Similarity 50.0%; Pred. No. 2.5e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEFPFXXE 10

Db 173 EIEAFFAAAE 182  
 RESULT 4  
 US-10-333-006-10  
 ; Sequence 10, Application US/10333006  
 ; Publication No. US20040019926A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Frankard, Valerie Marie-No. US20040019926A1lie S.  
 ; APPLICANT: Peres Bota, Adrian Marius  
 ; APPLICANT: Droual, Anne-Marie  
 ; APPLICANT: Mironov, Vladimir  
 ; APPLICANT: Inz., Dirk  
 ; APPLICANT: Hatzfeld, Yves  
 ; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS  
 ; FILE REFERENCE: 1187-13  
 ; CURRENT APPLICATION NUMBER: US/10/333,006  
 ; PRIOR FILING DATE: 2003-01-14  
 ; PRIOR APPLICATION NUMBER: PCT/IB01/01492  
 ; PRIOR FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/218,471  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: US 60/241,219  
 ; NUMBER OF SEQ ID NOS: 59  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 10  
 ; LENGTH: 262  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 US-10-333-006-10

Query Match 81.2%; Score 26; DB 15; Length 262;  
 Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEFPFXXE 10  
 DB 217 EIEAFFAAAE 226

RESULT 5  
 US-10-437-963-195115  
 ; Sequence 195115, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 195115  
 ; LENGTH: 417  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_91095C.1.pep  
 US-10-437-963-195115

Query Match 81.2%; Score 26; DB 16; Length 417;  
 Best Local Similarity 50.0%; Pred. No. 4.6e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEFPFXXE 10

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Db 372 EIEAFFAAAE 381
RESULT 6
US-10-333-006-13
; Sequence 13, Application US/10333006
; Publication No. US20040019926A1
; GENERAL INFORMATION:
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A1lle S.
; APPLICANT: Peres Bota, Adrian Marius
; APPLICANT: Droual, Anne-Marie
; APPLICANT: Mironov, Vladimir
; APPLICANT: Inz., Dirk
; APPLICANT: Hazfeld, Yves
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
; FILE REFERENCE: 1187-13
; CURRENT APPLICATION NUMBER: US/10/333,006
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: PCT/IB01/01492
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/218,471
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/241,219
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-333-006-13
Query Match 78.1%; Score 25; DB 15; Length 90;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10
Db 50 ELEAFFAAEE 59
RESULT 7
US-10-767-701-36263
; Sequence 36263, Application US/10767701
; Publication No. US20040172664A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 36263
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C86129_1.pep
US-10-767-701-36263
Query Match 78.1%; Score 25; DB 16; Length 95;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10
Db 54 EMEFFFAAE 63
RESULT 8
US-10-333-006-44
; Sequence 44, Application US/10333006
; Publication No. US20040019926A1
; GENERAL INFORMATION:
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A1lle S.
; APPLICANT: Peres Bota, Adrian Marius
; APPLICANT: Droual, Anne-Marie
; APPLICANT: Mironov, Vladimir
; APPLICANT: Inz., Dirk
; APPLICANT: Hazfeld, Yves
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
; FILE REFERENCE: 1187-13
; CURRENT APPLICATION NUMBER: US/10/333,006
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: PCT/IB01/01492
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/218,471
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/241,219
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-333-006-44
Query Match 78.1%; Score 25; DB 15; Length 194;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10
Db 154 ELEAFFAAEE 163
RESULT 9
US-10-437-963-120870
; Sequence 120870, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 120870
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_23950C.1.pep
US-10-437-963-120870
Query Match 78.1%; Score 25; DB 16; Length 194;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10
Db 154 ELEAFFAAEE 163
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RESULT 10  
US-10-424-599-182928  
; Sequence 182928, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 182928  
; LENGTH: 205  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_136198C.1.pep  
US-10-424-599-182928  
Query Match 78.1%; Score 25; DB 15; Length 205;  
Best Local Similarity 50.0%; Pred. No. 3.9e+02;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
| | | | |  
Db 164 EEEFFFAAE 173

RESULT 11  
US-10-437-963-128205  
; Sequence 128205, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 128205  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)...(218)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_30581C.1.pep  
US-10-437-963-128205  
Query Match 78.1%; Score 25; DB 16; Length 218;  
Best Local Similarity 60.0%; Pred. No. 4.1e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
| | | | |  
Db 180 EEEFFFAAE 189

RESULT 12  
US-10-425-114-59718  
; Sequence 59718, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 59718  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3732-047-G6\_FLI.pep  
US-10-425-114-59718  
Query Match 78.1%; Score 25; DB 15; Length 248;  
Best Local Similarity 50.0%; Pred. No. 4.7e+02;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
| | | | |  
Db 207 EMEFFFAAE 216

RESULT 13  
US-10-425-114-61054  
; Sequence 61054, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 61054  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3279-047-A7\_FLI.pep  
US-10-425-114-61054  
Query Match 78.1%; Score 25; DB 15; Length 255;  
Best Local Similarity 50.0%; Pred. No. 4.8e+02;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
| | | | |  
Db 214 EMEFFFAAE 223

RESULT 14  
US-10-369-493-22727  
; Sequence 22727, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 22727  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(401)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-10-369-493-22727

Query Match 78.1%; Score 25; DB 14; Length 401;  
Best Local Similarity 50.0%; Pred. No. 7.5e+02;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXE 10  
Db 351 ETESFFQAKE 360

RESULT 15  
US-10-369-493-22728  
; Sequence 22728, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 22728  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(401)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-10-369-493-22728

Query Match 78.1%; Score 25; DB 14; Length 401;  
Best Local Similarity 50.0%; Pred. No. 7.5e+02;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXE 10  
Db 351 ETESFFQAKE 360

Search completed: October 26, 2004, 15:33:30  
Job time : 144.846 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:27:13 ; Search time 13.8462 Seconds  
(without alignments)  
69.430 Million cell updates/sec

Title: US-09-574-735c-36  
Perfect score: 32  
Sequence: 1 EXEXFFXXE 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	78.1	62	2 B71318	conserved hypothetical
2	25	78.1	380	2 S62523	septin homolog - f
3	25	78.1	799	2 T02656	probable salt-indu
4	24	75.0	196	2 T09968	cyclin-dependent k
5	24	75.0	299	2 T15928	hypothetical prote
6	24	75.0	315	2 C83945	stage V sporulatio
7	24	75.0	660	2 A81704	DNA ligase TC0423
8	24	75.0	663	2 C71551	probable DNA ligas
9	24	75.0	786	2 T26811	hypothetical prote
10	24	75.0	808	2 T04092	phospholipase D (E
11	23	71.9	79	2 B81014	hypothetical prote
12	23	71.9	137	2 B86188	YUP8H12.5 (impor
13	23	71.9	140	2 C97710	nucleoside-diphosp
14	23	71.9	146	2 T71263	probable flavodoxi
15	23	71.9	146	2 A69950	conserved hypothet
16	23	71.9	155	2 T42687	hypothetical prote
17	23	71.9	191	2 T01132	cyclin-dependent k
18	23	71.9	200	2 AE1632	hypothetical prote
19	23	71.9	209	2 T46140	hypothetical prote
20	23	71.9	335	2 S76519	hypothetical prote
21	23	71.9	364	2 T20748	hypothetical prote
22	23	71.9	474	2 T31064	hypothetical prote
23	23	71.9	829	2 F75415	phosphoenolpyruvat
24	23	71.9	1251	2 A56677	neuronal cell cycl
25	23	71.9	1425	2 T22493	hypothetical prote
26	23	71.9	1673	2 T50806	complement compone
27	22	68.8	142	2 C82283	nucleoside diphosp
28	22	68.8	165	2 AB0851	hypothetical prote
29	22	68.8	165	2 S70217	sipE protein - Sal

sick protein - Sal  
hypothetical prote  
chromosome partiti  
hypothetical prote  
hypothetical prote  
conserved hypothet  
extragenic suppress  
extragenic suppress  
conserved hypothet  
calretinin - chick  
calretinin - human  
calretinin - rat  
p37NB - human  
UDP-N-acetylglucos  
two component sens  
nitrogen regulatio

ALIGNMENTS

RESULT 1

B71318  
conserved hypothetical protein TP0490 - syphilis spirochete  
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: B71318  
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi  
rson, J.; Khailak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; MCD  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A:Reference number: A71250; MUID:98332770; PMID:9665876  
A:Accession: B71318  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-62 <COL>  
A:Cross-references: UNIPROT:O83503; GB:AE001225; GB:AE000520; NID:G3322775; PIDN:AA6654  
A:Experimental source: strain Nichols  
C:Genetics:  
A:Gene: TP0490

Query Match 78.1%; Score 25; DB 2; Length 62;  
Best Local Similarity 50.0%; Pred. No. 9.8;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
DB 52 EAEDFFGSAE 61

RESULT 2

S62523  
septin homolog - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 16-May-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: T41191; T41431; T39129; S62523  
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.  
submitted to the EMBL Data Library, April 1999  
A:Reference number: Z21976  
A:Accession: T41191  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-380 <LYN>  
A:Cross-references: UNIPROT:Q09883; EMBL:AL049662; PIDN:CAB41232.1; GSPDB:GN00068; SPDB  
A:Experimental source: strain 972h; cosmid c188  
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, October 1998  
A:Reference number: Z21993  
A:Accession: T41431  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-380 <SEB>

A;Cross-references: EMBL:AL032824; PIDN:CA37422.1; GSPDB:GN00068; SPDB:SPCC584.09  
 A;Experimental source: strain 972h-; cosmid c584  
 R;Lye, G.; Churcher, C.M.; Barrall, B.G.; Rajandream, M.A.; Walsh, S.V.  
 submitted to the EMBL Data Library, November 1995

A;Reference number: Z21830  
 A;Accession: T39129  
 A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA  
 A;Residues: 1-380 <LY2>  
 A;Cross-references: EMBL:Z66569; NID:g1052533; PIDN:CAA91517.1; PID:g1052538; SPDB:SPACB

C;Genetics: <JfNI>  
 A;Gene: SPCC188.12  
 A;Map position: 3  
 A;Introns: 20/2

C;Genetics: <SEE2>  
 A;Gene: SPCC584.09  
 A;Map position: 3  
 A;Introns: 20/2

C;Genetics: <LY23>  
 A;Gene: SPDB:SPAC8A.07  
 A;Map position: 1  
 A;Introns: 20/2

C;Superfamily: Saccharomyces cerevisiae cell division control protein CDC10

Query Match 78.1%; Score 25; DB 2; Length 380;  
 Best Local Similarity 50.0%; Pred. No. 65;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
 DB 330 ETESFQAKE 339

RESULT 3  
 T02656  
 N;Alternate names: hypothetical protein [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004

A;Accession: T02656; H84664  
 R;Rounsley, S.D.; Ronning, C.M.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sy  
 submitted to the EMBL Data Library, August 1998

A;Description: Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence.  
 A;Reference number: Z14685  
 A;Accession: T02656

A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-799 <ROU>

A;Cross-references: UNIPROT:O81028; EMBL:AC005168; NID:g3426033; PID:g3426046  
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84664  
 A;Status: preliminary  
 A;Molecule type: DNA

A;Residues: 1-799 <STO>  
 A;Cross-references: GB:AB002093; NID:g3426046; PIDN:AAC32245.1; GSPDB:GN00139

C;Genetics:  
 A;Gene: F12C20.17; At2g26790  
 A;Map position: 2

Query Match 78.1%; Score 25; DB 2; Length 799;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
 DB 511 EAEDFFSLE 520

RESULT 6  
 C83945  
 stage V sporulation protein X BH2363 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans  
 C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
 C;Accession: C83945

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
 Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
 A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: C83945  
 A;Status: preliminary  
 A;Molecule type: DNA

A;Residues: 1-315 <STO>

## RESULT 4

T09968

cyclin-dependent kinase inhibitor protein - red goosefoot

C;Species: Chenopodium rubrum (red goosefoot)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C;Accession: T09968

R;Fountain, M.D.; Renz, A.; Beck, E.

submitted to the EMBL Data Library, November 1997

A;Description: A plant G1 cyclin-dependent kinase inhibitor gene from a photoautotrophic

A;Reference number: Z16910

A;Accession: T09968

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-196 &lt;FOU&gt;

A;Cross-references: UNIPROT:O48597; EMBL:AJ002173

A;Experimental source: photoautotrophic cells derived from hypocotyl tissue

C;Genetics:

A;Gene: CDK11

C;Keywords: protein kinase inhibitor

Query Match 75.0%; Score 24; DB 2; Length 196;

Best Local Similarity 50.0%; Pred. No. 58;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10

DB 155 EIEEPPAVAE 164

RESULT 5

T15928

hypothetical protein EEED8.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C;Accession: T15928

R;Chissee, S.

submitted to the EMBL Data Library, July 1995

A;Description: The sequence of C. elegans cosmid EEED8.

A;Reference number: Z18428

A;Accession: T15928

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-239 &lt;CHI&gt;

A;Cross-references: UNIPROT:Q09529; EMBL:U23484; NID:g733597; PID:g733599; PIDN:AAC46762

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CBSP.EEED8.2

A;Introns: 84/3; 133/3; 275/3

Query Match 75.0%; Score 24; DB 2; Length 299;

Best Local Similarity 50.0%; Pred. No. 91;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10

DB 134 EEESFFSLHE 143

RESULT 6

C83945

stage V sporulation protein X BH2363 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004

C;Accession: C83945

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: C83945

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-315 &lt;STO&gt;



```

A;Cross-references: UNIPROT:Q9KAC6; GB:BA000004; NID:g10174886; PIDN:BA0060
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2363
C;Superfamily: cfxQ protein

Query Match 75.0%; Score 24; DB 2; Length 315;
Best Local Similarity 50.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXE 10
Db 26 EEETFFHSEE 35

RESULT 7
A81704
DNA ligase TC0423 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 12-Jul-2004
C;Accession: A81704
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: A81704
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-660 <TET>
A;Cross-references: UNIPROT:Q9PKP2; GB:AE002309; GB:AE002160; NID:g7190464; PIDN:AAF3927
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0423
C;Superfamily: NAD+-dependent DNA ligase, Liga type

Query Match 75.0%; Score 24; DB 2; Length 660;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXE 10
Db 91 ELEEFFSRTE 100

RESULT 8
C71551
Probable DNA ligase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 12-Jul-2004
C;Accession: C71551
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: C71551
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-663 <ARN>
A;Cross-references: UNIPROT:O84148; GB:AE001288; GB:AE001273; NID:g3328545; PIDN:AAC6773
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: dnlg
C;Superfamily: NAD+-dependent DNA ligase, Liga type

Query Match 75.0%; Score 24; DB 2; Length 663;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXE 10
Db 91 ELEEFFSRTE 100

```

## RESULT 9

T26811  
 hypothetical protein Y41E3.4 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T26811  
 R;McMurray, A.  
 submitted to the EMBL Data Library, May 1997  
 A;Reference number: Z20270  
 A;Accession: T26811  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-786 <WIL>  
 A;Cross-references: UNIPROT:O62431; EMBL:Z95559; PIDN:CAB08998.1; GSPDB:GN000022; CBSP:Y  
 A;Experimental source: clone Y41E3  
 C;Genetics:

A;Gene: CBSP:Y41E3.4  
 A;Map position: 4  
 A;Introns: 83/3; 195/3; 357/3; 573/2; 749/2  
 C;Superfamily: human glutamine-tRNA ligase; glutamine-tRNA ligase homology

Query Match 75.0%; Score 24; DB 2; Length 786;  
 Best Local Similarity 50.0%; Pred. No. 2.5e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXE 10  
 Db 316 EEKFFSAIE 325

## RESULT 10

T04092  
 phospholipase D (EC 3.1.4.4) - common tobacco  
 C;Species: Nicotiana tabacum (common tobacco)  
 C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
 C;Accession: T04092  
 R;Lein, W.; Saalbach, G.  
 submitted to the EMBL Data Library, May 1997  
 A;Description: Characterization of tobacco phospholipase D.  
 A;Reference number: Z15203  
 A;Accession: T04092  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-808 <LEI>  
 A;Cross-references: UNIPROT:P93400; EMBL:Z84822; NID:e1057206; PIDN:CAB06620.1; PID:e33  
 A;Experimental source: strain SR1; tissue-type leaf  
 C;Superfamily: phospholipase D, plant type  
 C;Keywords: phosphoric diester hydrolase

Query Match 75.0%; Score 24; DB 2; Length 808;  
 Best Local Similarity 50.0%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXE 10  
 Db 293 ETEOFFQGTI 302

## RESULT 11

B81014  
 hypothetical protein NMB2037 [imported] - Neisseria meningitidis (strain MC58 serogroup  
 C;Species: Neisseria meningitidis  
 C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
 C;Accession: B81014; F81956  
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.  
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.  
 ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.  
 Science 287, 1809-1815, 2000  
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V  
 A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
 A;Reference number: A81000; MUID:20175755; PMID:10710307  
 A;Accession: B81014

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-79 <TET>  
A;Cross-references: UNIPROT:Q9JRC3; GB:AE002553; GB:AE002098; NID:G7227292; PIDN:AAF4235  
A;Experimental source: serogroup B, strain M58  
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
R;Holroyd, S.; Jagels, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
A;Reference number: A81775; MUID:20222556; PMID:10761919  
A;Accession: F81956  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-79 <PAR>  
A;Cross-references: GB:AL162753; GB:AL157959; NID:G7379120; PIDN:CAB83701.1; PID:G737915  
A;Experimental source: serogroup A, strain Z2491  
C;Genetics:  
A;Gene: NMB2037; NMA0401

Query Match 71.9%; Score 23; DB 2; Length 79;  
Best Local Similarity 50.0%; Pred. No. 41;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
| | | | |  
Db 61 EOEHFSEIE 70

RESULT 12  
B86188  
YUP8H12.5 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: B86188  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: B86188  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-137 <STO>  
A;Cross-references: UNIPROT:Q23036; GB:AE005172; NID:G2388563; PIDN:AAF71444.1; GSPDB:GN  
C;Genetics:  
A;Map position: 1

Query Match 71.9%; Score 23; DB 2; Length 137;  
Best Local Similarity 50.0%; Pred. No. 72;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
| | | | |  
Db 26 EAEDFVHVE 35

RESULT 13  
C97710  
nucleoside-diphosphate kinase (EC 2.7.4.6) [imported] - Rickettsia conorii (strain Malles  
C;Species: Rickettsia conorii  
C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 16-Aug-2004  
C;Accession: C97710  
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro  
Science 293, 2093-2098, 2001  
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A;Reference number: A37700; MUID:21442074; PMID:11557893  
A;Accession: C97710

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-140 <UR>  
A;Cross-references: UNIPROT:Q92JT4; GB:AE006914; PIDN:AAL02621.1; PID:G15619121; GSPDB:G  
C;Genetics:  
A;Gene: ndk  
C;Superfamily: Nucleoside diphosphate kinase  
C;Keywords: phosphotransferase

Query Match 71.9%; Score 23; DB 2; Length 140;  
Best Local Similarity 50.0%; Pred. No. 74;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
| | | | |  
Db 128 EIEFFNKSE 137

RESULT 14  
F71263  
Probable flavodoxin - syphilis spirochete  
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C;Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: F71263  
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin  
rson, J.; Khaliak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A;Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.  
A;Reference number: A71250; MUID:98332770; PMID:9665876  
A;Accession: F71263  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-146 <COL>  
A;Cross-references: UNIPROT:O83895; GB:AE001261; GB:AE000520; NID:G3323243; PIDN:AAC588  
A;Experimental source: strain Nichols  
C;Genetics:  
A;Gene: TP0925  
C;Superfamily: flavodoxin; flavodoxin homology  
C;Keywords: electron transfer; flavoprotein; FMN  
F;6-145/Domain: flavodoxin homology <FLX>

Query Match 71.9%; Score 23; DB 2; Length 146;  
Best Local Similarity 50.0%; Pred. No. 77;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
| | | | |  
Db 68 EPEFFTSIE 77

RESULT 15  
A69580  
Conserved hypothetical protein yqck - *Bacillus subtilis*  
C;Species: *Bacillus subtilis*  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: A69580  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Beter  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galler  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y. M.; Ogawa, K.; Ogiwara, A.; Oudaga, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A;Authors: Schleich, S.; Schroeder, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Seror  
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
A;Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: A69950  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-146 <KUN>  
A:Cross-references: UNIPROT:P45945; GB:Z99117; GB:AL009126; NID:G2634966; PIDN:CAB14521.  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: Yqck

Query Match 71.9%; Score 23; DB 2; Length 146;  
Best Local Similarity 50.0%; Pred. No. 77;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXEFFFFX 10  
Db 81 EXEGFFAREE 90

Search completed: October 26, 2004, 15:40:10  
Job time : 15.8462 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:27:03 ; Search time 55.7692 Seconds  
(without alignments)  
103.171 Million cell updates/sec

Title: US-09-574-735C-36  
Perfect score: 32  
Sequence: 1 EXEFFFFXXE 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	26	81.2	262	2	Q626G5	Q626G5 oryza sativ
2	26	81.2	262	2	BAD17213	BAD17213 oryza sat
3	25	78.1	62	2	O83503	O83503 treponema p
4	25	78.1	166	2	Q6T220	Q6T220 glycine max
5	25	78.1	166	2	AAS13377	AAS13377 glycine m
6	25	78.1	189	2	Q9LRY0	Q9LRY0 arabidopsis
7	25	78.1	192	2	Q9FS28	Q9FS28 pisum sativ
8	25	78.1	205	2	Q6T223	Q6T223 glycine max
9	25	78.1	205	2	AAS13374	AAS13374 glycine m
10	25	78.1	223	2	Q6LLB0	Q6LLB0 photobacter
11	25	78.1	223	2	CAG22039	CAG22039 photobact
12	25	78.1	242	2	Q7XDH8	Q7XDH8 oryza sativ
13	25	78.1	242	2	Q9FW65	Q9FW65 oryza sativ
14	25	78.1	293	2	Q92RW5	Q92RW5 rhizobium m
15	25	78.1	380	1	SPN6 SCHPO	O99883 schizosacch
16	25	78.1	436	2	Q8DZV3	Q8DZV3 streptococc
17	25	78.1	436	2	Q85KX1	Q85KX1 streptococc
18	25	78.1	618	2	C7S542	C7S542 neurospora
19	25	78.1	799	2	C81028	O81028 arabidopsis
20	24	75.0	123	2	Q6ZWH0	Q6ZWH0 homo sapien
21	24	75.0	123	2	BAC85533	BAC85533 homo sapi
22	24	75.0	148	2	Q67567	Q67567 digitaria s
23	24	75.0	185	2	Q8GT28	Q8GT28 lycopersico
24	24	75.0	196	2	C7RH53	C7RH53 plasmodium
25	24	75.0	196	2	C48597	C48597 chenopodium
26	24	75.0	198	2	Q6T222	Q6T222 glycine max
27	24	75.0	198	2	AAS13375	AAS13375 glycine m
28	24	75.0	210	2	Q8GT29	Q8GT29 lycopersico
29	24	75.0	222	2	O9FKB5	O9FKB5 arabidopsis
30	24	75.0	260	2	Q6C9I5	Q6C9I5 varrowia li
31	24	75.0	264	2	Q72U04	Q72U04 leptospira

32	24	75.0	264	2	Q8F150	Q8F150 leptospira
33	24	75.0	264	2	AAS69474	AAS69474 leptospir
34	24	75.0	299	1	YQO2 CAEEL	YQO2 caenorhabdi
35	24	75.0	315	2	Q9KAC6	Q9KAC6 bacillus ha
36	24	75.0	353	2	Q8S8B2	Q8S8B2 encephalito
37	24	75.0	370	2	Q7Q2A8	Q7Q2A8 anopheles g
38	24	75.0	439	1	GR65 HUMAN	GR65 homo sapien
39	24	75.0	445	1	GR65 MOUSE	GR65 mus musculu
40	24	75.0	445	2	Q7XV12	Q7XV12 oryza sativ
41	24	75.0	450	1	GR65 RAT	GR65 rattus norv
42	24	75.0	597	2	Q7Z4P8	Q7Z4P8 homo sapien
43	24	75.0	633	2	Q8NDL2	Q8NDL2 homo sapien
44	24	75.0	660	1	DNLJ CHLMU	DNLJ chlamydia m
45	24	75.0	663	1	DNLJ CHLTR	DNLJ chlamydia t

ALIGNMENTS

RESULT 1

Q626G5 PRELIMINARY; PRT; 262 AA.  
AC Q626G5; 05-JUL-2004 (T-EMBLrel. 27, Created)  
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
DE Hypothetical protein P0486G03.18.  
GN Name=P0486G03.18;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AP005002; BAD17213.1; -  
DR InterPro: IPR003175; CDI.  
DR Pfam: PF02234; CDI; 1.  
SQ Hypothetical protein.  
KW Hypothetical protein.  
SQ SEQUENCE 262 AA; 27138 MW; 42EC85C8276C0726 CRC64;

Query Match 81.2%; Score 26; DB 2; Length 262;  
Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEFFFFXXE 10

Db 217 EIEAFFAAAE 226

RESULT 2

BAD17213 PRELIMINARY; PRT; 262 AA.  
AC BAD17213; 10-MAY-2004 (T-EMBLrel. 27, Created)  
DT 10-MAY-2004 (T-EMBLrel. 27, Last sequence update)  
DT 10-MAY-2004 (T-EMBLrel. 27, Last annotation update)  
DE Hypothetical protein P0486G03.18.  
GN P0486G03.18.  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza; Oryza sativa.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=cv. Nipponbare;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RL "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC  
clone: P0486G03.18";  
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AP005002; BAD17213.1; -.
KW Hypothetical protein.
SQ SEQUENCE 262 AA; 27138 MW; 425C85C8276C0726 CRC64;

Query Match      81.2%; Score 26; DB 2; Length 262;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10
   |||||
Db 217 EIEAFFAAAE 226

RESULT 3
OB3503
ID O83503 PRELIMINARY; PRT; 62 AA.
AC O83503;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Hypothetical protein TP0490.
GN OrderedLocusNames=TP0490;
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Frazer C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R.J., Gwin M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,
RA Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,
RA Utterback T.R., McDonald L.A., Artach P., Bowman C., Cotton M.D.,
RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
RA Weidman J.F., Smith H.O., Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT Spirochete.";
RL Science 281:375-388(1998).
DR EMBL: AE001225; AAC65477.1; -.
DR PIR: B71318; B71318.
DR TIGR: TP0490; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 62 AA; 7230 MW; 6BD1E040146CFAD8 CRC64;

Query Match      78.1%; Score 25; DB 2; Length 62;
Best Local Similarity 50.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10
   |||||
Db 52 EAEDFFGSAAE 61

RESULT 4
Q87220
ID Q67220 PRELIMINARY; PRT; 166 AA.
AC Q67220;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein TP0490.
DE Cyclin-dependent kinase inhibitor 2;2 (Fragment).
OS Glycine max (Soybean)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RC SEQUENCE FROM N.A.
RA Li S., Reverdatto S., Nielsen N.C.;
RL Submitted (OCT-2003), to the EMBL/GenBank/DBJ databases.
DR EMBL: AY439104; AAS13377.1; -.
DR GO: GO:0016301; F:kinase activity; IEA.

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DR InterPro: IPR003175; CDI.
DR Pfam: PF02334; CDI; 1.
KW Cyclin; Kinase.
FT NON_TER 166
SQ SEQUENCE 166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;

Query Match      78.1%; Score 25; DB 2; Length 166;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10
   |||||
Db 127 ELEDFFAAAE 136

RESULT 5
AAS13377
ID AAS13377 PRELIMINARY; PRT; 166 AA.
AC AAS13377;
DT 10-MAY-2004 (TrEMBLrel. 27, Created)
DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Cyclin-dependent kinase inhibitor 2;2 (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RC SEQUENCE FROM N.A.
RA Li S., Reverdatto S., Nielsen N.C.;
RT "CDNA of cell-cycle genes in soybean cotyledons.";
RL Submitted (OCT-2003), to the EMBL/GenBank/DBJ databases.
DR EMBL: AY439104; AAS13377.1; -.
KW Cyclin; Kinase.
FT NON_TER 166
SQ SEQUENCE 166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;

Query Match      78.1%; Score 25; DB 2; Length 166;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10
   |||||
Db 127 ELEDFFAAAE 136

RESULT 6
Q9LRY0
ID Q9LRY0 PRELIMINARY; PRT; 189 AA.
AC Q9LRY0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similarity to cyclin-dependent kinase inhibitor protein (Cyclin-
DE dependent kinase inhibitor 5).
GN Name=krs5;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RC SEQUENCE FROM N.A.
RP MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

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RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21342510; PubMed=11449057;
RA de Veylder L., Beeckman T., Beemster G.T.S., Krols L., Terras F.,
RA Landrieu I., Van Der Schueren E., Maes S., Naudts M., Inze D.,
RT "Functional analysis of Cyclin-dependent kinase inhibitors of
RT Arabidopsis.",
RL Plant Cell 13:1653-1668(2001).
DR EMBL; AB028609; BAB02891.1; -.
DR EMBL; AJ301556; CAC1619.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
SQ SEQUENCE 189 AA; 21424 MW; A66041310E8DDE6 CRC64;

Query Match 78.1%; Score 25; DB 2; Length 189;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 148 EIEEFFASAE 157

RESULT 7
Q9FS28 PRELIMINARY; PRT; 192 AA.
AC Q9FS28;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cyclin dependent kinase inhibitor.
GN Name=cki;
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eursids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Axillary bud;
RA Shimizu-Sato S., Mori H.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB028483; BAB20860.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
SQ SEQUENCE 192 AA; 21921 MW; E76D734000885EB2 CRC64;

Query Match 78.1%; Score 25; DB 2; Length 192;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 151 EIEEFFASAE 160

RESULT 8
Q6T223 PRELIMINARY; PRT; 205 AA.
AC Q6T223;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cyclin-dependent kinase inhibitor 1;1.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eursids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RL Li S., Reverdatto S., Nielsen N.C.;
RA Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY439101; AAS13374.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
SQ SEQUENCE 205 AA; 22875 MW; 1B6F2D481710205E CRC64;

Query Match 78.1%; Score 25; DB 2; Length 205;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 164 ELEEFFAASE 173

RESULT 9
AAS13374 PRELIMINARY; PRT; 205 AA.
ID AAS13374;
AC AAS13374;
DT 10-MAY-2004 (TrEMBLrel. 27, Created)
DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Cyclin-dependent kinase inhibitor 1;1.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eursids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RL Li S., Reverdatto S., Nielsen N.C.;
RT "cDNA of cell-cycle genes in soybean cotyledons.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY439101; AAS13374.1; -.
KW Cyclin; Kinase.
SQ SEQUENCE 205 AA; 22875 MW; 1B6F2D481710205E CRC64;

Query Match 78.1%; Score 25; DB 2; Length 205;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 164 ELEEFFAASE 173

RESULT 10
Q6LLB0 PRELIMINARY; PRT; 223 AA.
ID Q6LLB0;
AC Q6LLB0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein YCAQ.
GN Name=YCAQ; OrderedLocusNames=PBRB0166;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74103;
RN [1]
RP SEQUENCE FROM N.A.

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RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,  
 RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,  
 RA Valle G.;  
 RT "Genome analysis of Photobacterium profundum reveals the complexity of  
 RT high pressure adaptations.";  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR378675; CAG22039.1; -;  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 223 AA; 25756 MW; F1DC29298B9C9C57 CRC64;

Query Match 78.1%; Score 25; DB 2; Length 223;  
 Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
 |||||  
 Db 189 EKETFFTALE 198

RESULT 11  
 CAG22039  
 ID CAG22039 PRELIMINARY; PRT; 223 AA.  
 AC CAG22039;  
 DT 10-MAY-2004 (TRENBLrel. 27, Created)  
 DT 10-MAY-2004 (TRENBLrel. 27, Last sequence update)  
 DT 10-MAY-2004 (TRENBLrel. 27, Last annotation update)  
 DE Hypothetical protein YCAQ.  
 GN YCAQ OR PBRB0166.  
 OS Photobacterium profundum (Photobacterium sp. (strain SS9)).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Photobacterium.  
 OX NCBI\_TaxID=74109;

RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,  
 RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,  
 RA Valle G.;  
 RT "Genome Analysis of Photobacterium profundum reveals the complexity of  
 RT high pressure adaptations.";  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR378675; CAG22039.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 223 AA; 25756 MW; F1DC29298B9C9C57 CRC64;

Query Match 78.1%; Score 25; DB 2; Length 223;  
 Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
 |||||  
 Db 189 EKETFFTALE 198

RESULT 12  
 Q7XDH8  
 ID Q7XDH8 PRELIMINARY; PRT; 242 AA.  
 AC Q7XDH8;  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Putative cyclin-dependent kinase inhibitor.  
 GN ORNames=OSUNB0094K03.16;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzae; Oryza.  
 OX NCBI\_TaxID=39947;

RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,  
 RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,  
 RA Valle G.;  
 RT "Genome analysis of Photobacterium profundum reveals the complexity of  
 RT high pressure adaptations.";  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR378675; CAG22039.1; -;  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 223 AA; 25756 MW; F1DC29298B9C9C57 CRC64;

Query Match 78.1%; Score 25; DB 2; Length 223;  
 Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
 |||||  
 Db 189 EKETFFTALE 198

RESULT 13  
 Q9FW65  
 ID Q9FW65 PRELIMINARY; PRT; 242 AA.  
 AC Q9FW65;  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Putative cyclin-dependent kinase inhibitor.  
 GN Names=OSUNB0094K03.16;  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzae; Oryza.  
 OX NCBI\_TaxID=4530;

RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,  
 RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,  
 RA Valle G.;  
 RT "Genome Analysis of Photobacterium profundum reveals the complexity of  
 RT high pressure adaptations.";  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR378675; CAG22039.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 223 AA; 25756 MW; F1DC29298B9C9C57 CRC64;

Query Match 78.1%; Score 25; DB 2; Length 242;  
 Best Local Similarity 50.0%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
 |||||  
 Db 202 ELEAFPAEE 211

RESULT 13  
 Q9FW65  
 ID Q9FW65 PRELIMINARY; PRT; 242 AA.  
 AC Q9FW65;  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Putative cyclin-dependent kinase inhibitor.  
 GN Names=OSUNB0094K03.16;  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzae; Oryza.  
 OX NCBI\_TaxID=4530;

RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,  
 RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,  
 RA Valle G.;  
 RT "Genome Analysis of Photobacterium profundum reveals the complexity of  
 RT high pressure adaptations.";  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR378675; CAG22039.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 223 AA; 25756 MW; F1DC29298B9C9C57 CRC64;

Query Match 78.1%; Score 25; DB 2; Length 223;  
 Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
 |||||  
 Db 189 EKETFFTALE 198

RESULT 12  
 Q7XDH8  
 ID Q7XDH8 PRELIMINARY; PRT; 242 AA.  
 AC Q7XDH8;  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Putative cyclin-dependent kinase inhibitor.  
 GN ORNames=OSUNB0094K03.16;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzae; Oryza.  
 OX NCBI\_TaxID=39947;

Query Match 78.1%; Score 25; DB 2; Length 242;  
 Best Local Similarity 50.0%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
 |||||  
 Db 202 ELEAFPAEE 211

RESULT 13  
 Q9FW65  
 ID Q9FW65 PRELIMINARY; PRT; 242 AA.  
 AC Q9FW65;  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Putative cyclin-dependent kinase inhibitor.  
 GN Names=OSUNB0094K03.16;  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzae; Oryza.  
 OX NCBI\_TaxID=4530;

RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,  
 RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,  
 RA Valle G.;  
 RT "Genome Analysis of Photobacterium profundum reveals the complexity of  
 RT high pressure adaptations.";  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR378675; CAG22039.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 223 AA; 25756 MW; F1DC29298B9C9C57 CRC64;

Query Match 78.1%; Score 25; DB 2; Length 242;  
 Best Local Similarity 50.0%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10  
 |||||  
 Db 202 ELEAFPAEE 211



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RESULT 14
Q92RW5 PRELIMINARY; PRT; 293 AA.
AC Q92RW5;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.
GN OrderedLocustNames=R00725; ORFNames=SMC00780;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1021;
RX MEDLINE=21368234; PubMed=11474104;
RA Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
RA Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
RA Cloux A., Davis R.W., Dreano S., Pederspiel N.A., Fisher R.F.,
RA Gloux S., Godrie T., Goffeau A., Golding B., Guzy J., Gurjal M.,
RA Hernandez-Lucas T., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
RA Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,
RA Verhoeveler F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
RT "The composite genome of the legume symbiont Sinorhizobium meliloti";
RL Science 293:668-672(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=1021;
RX MEDLINE=21368234; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Guzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591784; CAC45297.1; -.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PROSITE; PS50931; HTH_LYSR; 1.
KW Complete proteome.
SQ SEQUENCE 293 AA; 32763 MW; BF6530C41BF9245A CRC64;

Query Match 78.1%; Score 25; DB 2; Length 293;
Best Local Similarity 50.0%; Pred.No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXE 10
Db 60 EGEVFFAAAE 69

RESULT 15
SPN6.SCHPO
ID SPN6 SCHPO STANDARD; PRT; 380 AA.
AC Q09883;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Septin homolog spn6.
GN Name=spn6; ORFNames=SPCC188.12, SPCC584.09;

Query Match 78.1%; Score 25; DB 1; Length 380;
Best Local Similarity 50.0%; Pred.No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXE 10
Db 330 ETESFFQAKE 339

Search completed: October 26, 2004, 15:39:29

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OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Scours J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.W.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Woltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lenrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas R., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
RN [2]
RP CHARACTERIZATION.
RA Wu J.-Q., Pringle J.R.; to Swiss-Prot.
RA Submitted (MAR-2001) to Swiss-Prot.
CC -!- FUNCTION: Sporulation specific protein.
CC -!- SUBCELLULAR LOCATION: Cortices of developing spores.
CC -!- SIMILARITY: Belongs to the septin family.
CC -----
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CC -----
DR EMBL; AL032824; CAB37422.1; -.
DR EMBL; AL049662; CAB41232.1; -.
DR PIR; T41191; S62523.
DR GeneDB SPombe; SPCC188.12; -.
DR InterPro; IPR000038; GTP_Cell_Div.
DR Pfam; PF00735; GTP_CDC; 1.
DR ProDom; PD02565; GTP_Cell_Div; 1.
KW Cell division; Coiled coil; GTP-binding; Sporulation.
FT NP_BIND 37 44 GTP (Potential).
FT DOMAIN 304 380 Coiled coil (Potential).
SQ SEQUENCE 380 AA; 44011 MW; 450D86AEBC2BC8F CRC64;

Query Match 78.1%; Score 25; DB 1; Length 380;
Best Local Similarity 50.0%; Pred.No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXE 10
Db 330 ETESFFQAKE 339

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Wed Oct 27 09:35:41 2004

us-09-574-735c-36.rup

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Job time : 57.7692 secs